

SEQUENCE LISTING

<110> University of Utah Research Foundation

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<120> Mu-Conopeptides

<130> 2314-242

<150> US 60/219,619

<151> 2000-07-21

<150> US 60/245,157

<151> 2000-11-03

<150> US 60/264,319

<151> 2001-01-29

<150> US 60/277,270

<151> 2001-03-21

<160> 520

<170> PatentIn version 3.0

<210> 1

<211> 280

<212> DNA

<213> Conus arentus

<400> 1

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agagcgtatg caggacgact ttataactga gcatcatccc ctgtttgacg ctgtcaaacg 180

gtgttgcgag aggccatgca acataggatg cgtaccttgt tgtaaatgac cagctttgtc 240

atcgccgcct catcaagcga ataagtaaaa cgattgcagt 280

<210> 2

<211> 67

<212> PRT

<213> Conus arentus

<400> 2

Met Met Ser Lys Leu Gly Val Phe Leu Thr Ile Cys Met Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Phe Ile Thr Glu His His Pro Leu Phe

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35          40          45
Asp Pro Val Lys Arg Cys Cys Glu Arg Pro Cys Asn Ile Gly Cys Val
50          55          60

Pro Cys Cys
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<210> 3
<211> 14
<212> PRT
<213> Conus arentus

<220>
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<222> (1)..(14)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 an
d 12 is Pro or Hy

<400> 3
Cys Cys Xaa Arg Xaa Cys Asn Ile Gly Cys Val Xaa Cys Cys
1          5          10

<210> 4
<211> 244
<212> DNA
<213> Conus atlanticus

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actgctcttc cgctggatga agatcaaccg gtacaccgac ctgcagagcg tatgcaggac 120
atttcattctg atcaacatct cttctttgat ctcataaac ggtgctgcga gttgccatgc 180
gggccaggct tttgcgtccc ttgttgcctga catcaataac gtgttgatga ccaactttct 240
cgag 244

<210> 5
<211> 69
<212> PRT
<213> Conus atlanticus

<400> 5
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1          5          10          15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His
20          25          30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe
35          40          45

Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe
50          55          60

Cys Val Pro Cys Cys
65

<210> 6
<211> 15
<212> PRT
<213> Conus atlanticus

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<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8
 and 13 is Pro or Hy

<400> 6
 Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys
 1 5 10 15

<210> 7
 <211> 310
 <212> DNA
 <213> Conus aurisiacus

<400> 7
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 agagcgtatg caggacgaca ttcatctga gcagcatccc ttgtttaatc agaaaagaat 180
 gtgttgcggc gaaggccgga aatgccccag ctatttcaga aacagtcaaga ttgtcattg 240
 ttgttaaagt acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa 300
 cgattgcagt 310

<210> 8
 <211> 74
 <212> PRT
 <213> Conus aurisiacus

<400> 8
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
 20 25 30
 Glu Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe
 35 40 45
 Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr
 50 55 60
 Phe Arg Asn Ser Gln Ile Cys His Cys Cys
 65 70

<210> 9
 <211> 22
 <212> PRT
 <213> Conus aurisiacus
 <220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i
 s Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 9
 Met Cys Cys Gly Xaa Gly Arg Lys Cys Xaa Ser Xaa Phe Arg Asn Ser
 1 5 10 15

Gln Ile Cys His Cys Cys

20

<210> 10
 <211> 257
 <212> DNA
 <213> Conus aurisiacus

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 gacatttcat ctgagcagca tcgcttggtc aatcagaaaa gaaggtgctg ccggtggcca 180
 tgccccgcac aaatcgacgg tgaatatgtg ggtgtgtgcc ttggatgata accgtgttga 240
 tgaccaactt tctcgag 257

<210> 11
 <211> 75
 <212> PRT
 <213> Conus aurisiacus

<400> 11
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Pro Ile Asp Gly Asp Gln Ser Val Asp
 20 25 30
 Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Arg
 35 40 45
 Leu Phe Asn Gln Lys Arg Arg Cys Cys Arg Trp Pro Cys Pro Arg Gln
 50 55 60
 Ile Asp Gly Glu Tyr Cys Gly Cys Cys Leu Gly
 65 70 75

<210> 12
 <211> 19
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 3 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 12
 Cys Cys Arg Xaa Xaa Cys Xaa Arg Gln Ile Asp Gly Xaa Xaa Cys Gly
 1 5 10 15
 Cys Cys Leu

<210> 13
 <211> 262
 <212> DNA
 <213> Conus aurisiacus

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actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120
gacatttcac ctgagcagta tcccttggtt gataagagac aaaagtgttg cactgggaag 180
aaggggtcat gtcocggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240
gttgatgacc aactttctcg ag 262

<210> 14
<211> 78
<212> PRT
<213> Conus aurisiacus

<400> 14
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15
Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp
20 25 30
Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro
35 40 45
Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys
50 55 60
Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
65 70 75

<210> 15
<211> 23
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu

<400> 15
Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
1 5 10 15
Lys Asn Leu Lys Cys Cys Ser
20

<210> 16
<211> 232
<212> DNA
<213> Conus aurisiacus

<400> 16
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actgctgttc cgctggatgg agatcaacct ctgaccgcac acgcggagcg tatgcatgat 120
ggcattttcac ctaaaacgca tccctgggtt gatcccgta aacggtgttg caaggtgcaa 180
tgcgagtctt gcaccctctg ttgctaacgt gttgatgacc aactttctcg ag 232

<210> 17
<211> 68
<212> PRT
<213> Conus aurisiacus

<400> 17
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Leu Asp
 20 25 30
 Arg His Ala Glu Arg Met His Asp Gly Ile Ser Pro Lys Arg His Pro
 35 40 45
 Trp Phe Asp Pro Val Lys Arg Cys Cys Lys Val Gln Cys Glu Ser Cys
 50 55 60
 Thr Pro Cys Cys
 65
 <210> 18
 <211> 13
 <212> PRT
 <213> Conus aurisiacus
 <220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 11 i
 s Pro or Hyp
 <400> 18
 Cys Cys Lys Val Gln Cys Xaa Ser Cys Thr Xaa Cys Cys
 1 5 10
 <210> 19
 <211> 241
 <212> DNA
 <213> Conus bandus
 <400> 19
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 gtttcatctg aacagcatcc cttgtttgat cccgtcaaac ggtgttgcaa ctggccatgc 180
 tccatgggat gcatcccttg ttgctactat taataacgtg ttgatgacca actttctcga 240
 g 241
 <210> 20
 <211> 70
 <212> PRT
 <213> Conus bandus
 <400> 20
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp
 20 25 30
 Arg Pro Ala Glu Arg Ser Gln Asp Val Ser Ser Glu Gln His Pro Leu
 35 40 45
 Phe Asp Pro Val Lys Arg Cys Cys Asn Trp Pro Cys Ser Met Gly Cys
 50 55 60

Ile Pro Cys Cys Tyr Tyr
65 70

<210> 21
<211> 16
<212> PRT
<213> Conus bandus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp; Xaa at residue 15 and 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 21
Cys Cys Asn Xaa Xaa Cys Ser Met Gly Cys Ile Xaa Cys Cys Xaa Xaa
1 5 10 15

<210> 22
<211> 298
<212> DNA
<213> Conus betulinus

<400> 22
caagaggggat c gatagcagt tcatgatgtc taaactggga gtcttgttga ccttctgtct 60
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agagcgtatg caggacattt catctgaaca gcaccccttg ttgatcccg tcaaacgggtg 180
ttgcgaattg ccatgccatg gatgcgtccc ttgttgctgg ccttaataac gtgtggatga 240
ccaactgtgt tatcaaggcc acgtcaagtg tctaataaat aagtaaaatg attgcagt 298

<210> 23
<211> 67
<212> PRT
<213> Conus betulinus

<400> 23
Met Met Ser Lys Leu Gly Val Leu Leu Thr Phe Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ser Ser Glu Gln His Pro Leu Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Glu Leu Pro Cys His Gly Cys Val Pro Cys
50 55 60

Cys Trp Pro
65

<210> 24
<211> 15
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 1

1 and 15 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp

<400> 24

Cys Cys Xaa Leu Xaa Cys His Gly Cys Val Xaa Cys Cys Xaa Xaa
1 5 10 15

<210> 25

<211> 298

<212> DNA

<213> Conus betulinus

<400> 25

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agagcgtatg caggacattt cacctgaaca gcatccctog ttgatcccg tcaaacgggtg 180

ttggcggctg ccatgcaatg gatgcgtccc ttgttgctgg ccttcataac gtgtggacga 240

ccaactttgt tatcacggcc acgtcaagt tctgatgaat aagtaaaacg attgcagt 298

<210> 26

<211> 68

<212> PRT

<213> Conus betulinus

<400> 26

Met Met Ser Lys Leu Gly Val Leu Leu Thr Phe Cys Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg His
20 25 30

Ala Glu Arg Met Gln Asp Ile Ser Pro Glu Gln His Pro Ser Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Gly Leu Pro Cys Asn Gly Cys Val Pro Cys
50 55 60

Cys Trp Pro Ser

65

<210> 27

<211> 16

<212> PRT

<213> Conus betulinus

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 5, 11 and 15 is Pro or Hyp; Xaa at residue 14 is T
rp or bromo-Tr

<400> 27

Cys Cys Gly Leu Xaa Cys Asn Gly Cys Val Xaa Cys Cys Xaa Xaa Ser
1 5 10 15

<210> 28

<211> 282

<212> DNA

<213> Conus betulinus

<400> 28

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 gtgctgctcg aggaactgcg cagtatgcat ccttgttgc ccgaattggc cagcttgatt 240
 atcgcggcca agagtctaag gaataagtaa aacgattgca gt 282

<210> 29
 <211> 71
 <212> PRT
 <213> Conus betulinus

<400> 29
 Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Tyr Met Leu Leu Phe
 1 5 10 15

Pro Phe Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

Leu Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Val Asn Pro Trp Phe
 35 40 45

Asp Pro Val Lys Arg Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Pro
 50 55 60

Cys Cys Pro Asn Trp Pro Ala
 65 70

<210> 30
 <211> 18
 <212> PRT
 <213> Conus betulinus

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 11, 14 and 17 is Pro or Hyp; Xaa at residue 16 is
 Trp or bromo-Tr

<400> 30
 Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa Asn Xaa
 1 5 10 15

Xaa Ala

<210> 31
 <211> 325
 <212> DNA
 <213> Conus bullatus

<400> 31
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 agagcgctatg caggacgaca ttcatctga gcagaattcc ttgcttgaga agagagttac 180
 tgacaggtgc tgcaaaaggga agagggaatg cggcagatgg tgcagagatc actcgcgttg 240
 ttgcggtcga cgataagctg ttgatgacca gctttgttat caccgctaca tcaagtgtct 300
 agtgaataag taaaatgatt gcagt 325

<210> 32

<211> 77
 <212> PRT
 <213> Conus bullatus

<400> 32
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Ser Leu Leu
 35 40 45
 Glu Lys Arg Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Glu Cys Gly
 50 55 60
 Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
 65 70 75

<210> 33
 <211> 23
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 11 is Glu or gamma-carboxy Glu; Xaa at residue 15
 is Trp or bromo-Tr

<400> 33
 Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Xaa Cys Gly Arg Xaa Cys
 1 5 10 15
 Arg Asp His Ser Arg Cys Cys
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<210> 34
 <211> 326
 <212> DNA
 <213> Conus bullatus

<400> 34
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 agagcgtatg caggatgaca ttcatctga gcagaatccc ttgcttgaga agagagttgg 180
 tgacagggtc tgcaaaagga agaggggggtg cggcagatgg tgcagagatc actcacgttg 240
 ttgcgggtcga cgataacgtg ttgatgacca gctttgttat cacggctaca tcaagtgtct 300
 tagtgattaa gtaaaacgat tgcagt 326

<210> 35
 <211> 77
 <212> PRT
 <213> Conus bullatus

<400> 35
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Phe Ala Leu Arg Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Pro Leu Leu
35 40 45

Glu Lys Arg Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly
50 55 60

Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
65 70 75

<210> 36

<211> 23

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 15 is Trp or bromo-Trp

<400> 36

Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly Arg Xaa Cys
1 5 10 15

Arg Asp His Ser Arg Cys Cys
20

<210> 37

<211> 331

<212> DNA

<213> Conus bullatus

<400> 37

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gtttctgttt cccctttttg ctcttcgcga ggatggagat caacctgcag accgacctgc 120

agagcgtatg caggacgaca ttcatctga gcagaatccc ttgcttgaga agagagttgg 180

tgaaaggtgc tgcaaaaacg ggaagagggg gtgcggcaga tggtcagag atcactcacg 240

ttgttcggtg cgacgataac gtgttgatga ccgaggttt cgttatcacg gctacatcaa 300

gtgtctagtg aataagtaaa acgattgcag t 331

<210> 38

<211> 78

<212> PRT

<213> Conus bullatus

<400> 38

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Pro Leu Leu
35 40 45

Glu Lys Arg Val Gly Glu Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys
50 55 60

Gly Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg

65

70

75

<210> 39
 <211> 24
 <212> PRT
 <213> *Conus bullatus*

 <220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 16 i
 s Trp or bromo-Tr

<400> 39
 Val Gly Xaa Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys Gly Arg Xaa
 1 5 10 15

Cys Arg Asp His Ser Arg Cys Cys
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<210> 40
 <211> 337
 <212> DNA
 <213> *Conus bullatus*

 <400> 40
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 agagcgatatg caggacgacc ttctcatctga gcagcatccc ttgtttgaga agagaattgt 180
 tgacagggtgc tgcaacaaag ggaacgggaa gaggggggtgc agcagatggt gcagagatca 240
 ctcacgttgt tgccggtcgac gatgaactgt tgatgaccga ggcttttggtt atcacggcta 300
 catcaagtgt ctagtgaata agtaaaacga ttgcagt 337

<210> 41
 <211> 80
 <212> PRT
 <213> *Conus bullatus*

<400> 41
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe
 35 40 45

Glu Lys Arg Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg
 50 55 60

Gly Cys Ser Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
 65 70 75 80

<210> 42
 <211> 26
 <212> PRT
 <213> *Conus bullatus*

<220>

<221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 18 is Trp or bromo-Trp

<400> 42
 Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg Gly Cys Ser
 1 5 10 15

Arg Xaa Cys Arg Asp His Ser Arg Cys Cys
 20 25

<210> 43
 <211> 337
 <212> DNA
 <213> Conus bullatus

<400> 43
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 gcttctgttt cccctttttg ctcttcgcga ggatggagat caacctgcag accgacctgc 120
 tgagcgtatg caggacgaca ttcatctga gcggaatccc ttgtttgaga agagcgttgg 180
 tttatatctg tgcgcaccca aacccaacgg gcagatgatg tgcgcacagat ggtgcgaaaa 240
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 catcaagtat ctagtgaata agtaaaacga ttgcagt 337

<210> 44
 <211> 77
 <212> PRT
 <213> Conus bullatus

<400> 44
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asn Pro Leu Phe Glu Lys
 35 40 45

Ser Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp
 50 55 60

Arg Trp Cys Glu Lys Asn Ser Arg Cys Cys Gly Arg Arg
 65 70 75

<210> 45
 <211> 27
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 21 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 19 is Trp or bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 45
 Val Gly Leu Xaa Cys Cys Arg Xaa Lys Xaa Asn Gly Gln Met Met Cys

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1              5              10              15
Asp Arg Xaa Cys Xaa Lys Asn Ser Arg Cys Cys
      20              25

<210> 46
<211> 323
<212> DNA
<213> Conus bullatus
<400> 46
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agaacgtatg caggacgacc ttcatctga gcagcatccc ttgtttgttc agaaaagaag      180
gtgttgcggc gaaggcttga catgccccag atattggaaa aacagtcaga ttgtgtgttg      240
ttgttaaatg acaacgtgtc gatgaccaac ttcggtatca cgactacgcc aagtgtctaa      300
tgaataagta aaacgattgc agt                                          323

<210> 47
<211> 74
<212> PRT
<213> Conus bullatus

<400> 47
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1              5              10              15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
      20              25              30

Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe
      35              40              45

Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr
      50              55              60

Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys
65              70

<210> 48
<211> 22
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i
s Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at resid
ue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
or O-phospho-Ty

<400> 48
Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser
1              5              10              15

Gln Ile Cys Ala Cys Cys
      20

<210> 49
<211> 322

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<212> DNA
<213> Conus bullatus

<400> 49
caagagggat cgatagcagt tcatgatgtc taaactggca gtcttggtga ccactctgtc 60
gtctctgttt cccctttttg ctcttcgcga ggatggagat caacctgcag accgacctgc 120
tgagcgtatg caggacgaca ttcatctga gcaggatccc ttgtttgttc agaaaagaag 180
gtgttgccgc gaaggcttga catgcccag atattggaaa aacagtcaga ttgtgcttg 240
ttgttaaatg acaacgtgtg atgaccaact tggatatcac gactacgcca agtgtcta 300
gaataagtaa aacgattgca gt 322

<210> 50
<211> 74
<212> PRT
<213> Conus bullatus

<400> 50
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15
Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asp Pro Leu Phe
35 40 45
Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr
50 55 60
Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys
65 70

<210> 51
<211> 22
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 is
s Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at resid
ue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
or O-phospho-Tyr

<400> 51
Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser
1 5 10 15
Gln Ile Cys Ala Cys Cys
20

<210> 52
<211> 238
<212> DNA
<213> Conus capitaneus

<400> 52
ggatccatga tgtctaaact gggagtcttg gtgaccatct gctgtctttt gtttccctt 60
gctgtctttt cactggatgg aaatcaacct gcagaccacc ctgcaaagcg tacgcaagat 120

gacagttcag ctgccctgat caatacctgg attgatcatt cccattcttg ctgcaggagc 180
 tgcggtgaag attgtgttg ttgttgccgg taacgtgttg atgaccaact ttctcgag 238

<210> 53
 <211> 70
 <212> PRT
 <213> Conus capitaneus

<400> 53
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asn Gln Pro Ala Asp
 20 25 30
 His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn
 35 40 45
 Thr Trp Ile Asp His Ser His Ser Cys Cys Arg Asp Cys Gly Glu Asp
 50 55 60
 Cys Val Gly Cys Cys Arg
 65 70

<210> 54
 <211> 15
 <212> PRT
 <213> Conus capitaneus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 8 is Glu or gamma-carboxy Glu

<400> 54
 Ser Cys Cys Arg Asp Cys Gly Xaa Asp Cys Val Gly Cys Cys Arg
 1 5 10 15

<210> 55
 <211> 323
 <212> DNA
 <213> Conus characteristicus

<400> 55
 caagagggat cgaatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60
 gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120
 agatcgtatg caggacgaca ttcatctga gcagtatccc ttgtttgata tgagaaaaag 180
 gtgttgccgc ccggcggtt catgccccgt atatttcaga gacaatttta ttgtgtgttg 240
 ttgttaaatg acaactgtgc gatgaaccaac ttattatca cgactacgcc aagtgtctaa 300
 tgaataagta aaatgattgc agt 323

<210> 56
 <211> 74
 <212> PRT
 <213> Conus characteristicus

<400> 56

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 57
<211> 21
<212> PRT
<213> Conus characteristicus

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 11 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 57
Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe
1 5 10 15

Ile Cys Gly Cys Cys
20

<210> 58
<211> 316
<212> DNA
<213> Conus characteristicus

<400> 58
caagagggat cgaatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
gctctgtgtt ccccttactg ctcttccgat ggatggagat gaacctgcaa accgacctgt 120
cgagcgtatg caggacaaca ttcatctga gcagtatccc ttgtttgaga agagacgaga 180
ttgttgcaact ccgccaaga aatgcaaaga ccgacaatgc aaaccccaga gatgttgccg 240
tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgtt tagtgaataa 300
gtaaaatgat tgcagt 316

<210> 59
<211> 75
<212> PRT
<213> Conus characteristicus

<400> 59
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe

35 40 45
 Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
 50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
 65 70 75

<210> 60
 <211> 22
 <212> PRT
 <213> Conus characteristic

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 60
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
 1 5 10 15

Xaa Gln Arg Cys Cys Ala
 20

<210> 61
 <211> 314
 <212> DNA
 <213> Conus characteristic

<400> 61
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60
 gcttctgttt ccccttactg ctcttccact ggatggagat caacctgcag atcaatctgc 120
 agagcgacct gcagagcgta cgcaggacga cattcagcag catccgttat atgatccgaa 180
 aagaaggtgt tgccgttatc catgccccga cagctgccac ggatcttctgt gctataagtg 240
 ataacatgtt gatggccagc ttgttatca cggccacgtc aagtgtctta atgaataagt 300
 aaaacgattg cagt 314

<210> 62
 <211> 72
 <212> PRT
 <213> Conus characteristic

<400> 62
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ser
 20 25 30
 Ala Glu Arg Pro Ala Glu Arg Thr Gln Asp Asp Ile Gln Gln His Pro
 35 40 45

Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser
 50 55 60

Cys His Gly Ser Cys Cys Tyr Lys
 65 70

<210> 63
 <211> 18

<212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 and 17 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
 pho-Ty

<400> 63
 Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys
 1 5 10 15

Xaa Lys

<210> 64
 <211> 292
 <212> DNA
 <213> Conus characteristicus

<400> 64
 caagagggat cgaatagcagt tcatgatgtc taaactggga gccttggtga ccatctgtct 60
 acttctgttt tccctactag ctgttccgct ggatggagat caacatgcag accaacctgc 120
 acagcgtctg caggaccgca ttccaactga agatcatccc ttatttgatc ccaacaaacg 180
 gtgttgcccg ccggtggcat gcaacatggg atgcaagcct tgttggtgat gaccagcttt 240
 gttatcgcgg tcttcatgaa gtgtcttaat gaataagtaa aatgattgca gt 292

<210> 65
 <211> 69
 <212> PRT
 <213> Conus characteristicus

<400> 65
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30

Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
 35 40 45

Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys
 50 55 60

Lys Pro Cys Cys Gly
 65

<210> 66
 <211> 15
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 3, 4 and 13 is Pro or Hyp

<400> 66
 Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys

1 5 10 15

<210> 67
 <211> 293
 <212> DNA
 <213> Conus characteristicus

<400> 67
 caagagggat cgaatagcagt tcatgatgtc taaactggga gccttggtga ccattctgtct 60
 acttctgttt tcoctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120
 agagcgtctg catgaccgcc ttccaactga aaatcattcc ttatatgac ccgtcaaacg 180
 gtgttgogat gattcggaat gcgactattc ttgctggcct tgctgtatgt ttggataaac 240
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 68
 <211> 71
 <212> PRT
 <213> Conus characteristicus

<400> 68
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
 50 55 60
 Trp Pro Cys Cys Met Phe Gly
 65 70

<210> 69
 <211> 17
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is
 Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue
 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
 O-phospho-Ty

<400> 69
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
 1 5 10 15

Phe

<210> 70
 <211> 232
 <212> DNA
 <213> Conus characteristicus

<400> 70
 ggatccatga tgtctaaact gggagtcttg ttgacctct gtctgtctct gtttccctt 60

actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taagcaggac 120
 gtttcactcg aacagcatcc cttctttgat cccgtcaaac ggtgttgccg ccggtgttac 180
 atgggatgca tcccttggtg cttttaacgt gttgatgacc aactttctcg ag 232

<210> 71
 <211> 68
 <212> PRT
 <213> Conus characteristicus

<400> 71
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Arg Pro Ala Glu Arg Lys Gln Asp Val Ser Ser Glu Gln His Pro Phe
 35 40 45

Phe Asp Pro Val Lys Arg Cys Arg Arg Cys Tyr Met Gly Cys Ile
 50 55 60

Pro Cys Cys Phe
 65

<210> 72
 <211> 14
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 72
 Cys Cys Arg Arg Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
 1 5 10
 <210> 73
 <211> 323
 <212> DNA
 <213> Conus circumcicus

<400> 73
 caagaaggat cgaatagcagt tcatgatgtc taaactgggg gtattgttga ccatctgtct 60
 gttctgtgtt ccccttactg ctcttccaat ggaatggagat caacctgcag accaactgc 120
 agatcgtatg caggacgaca ttctatctga gcagtatccc ttgtttgata agagacgaaa 180
 gtgttgccgc aaagacgggc catgccocaa atatttcaaa gacaatttta ttgtgtgttg 240
 ttgtttaaag acaactgtgc gatgaccaac ttctgtatca cgattcgcca agtgtcttaa 300
 tgaataagta aaatgattgc agt 323

<210> 74
 <211> 74
 <212> PRT
 <213> Conus circumcicus

<400> 74
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30
 Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
 35 40 45
 Asp Lys Arg Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr
 50 55 60
 Phe Lys Asp Asn Phe Ile Cys Gly Cys Cys
 65 70

<210> 75
 <211> 23
 <212> PRT
 <213> Conus circumciscus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 9 and 11 is Pro or Hyp; Xaa at residue 13 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
 y

<400> 75
 Arg Lys Cys Cys Gly Lys Asp Gly Xaa Cys Xaa Lys Xaa Phe Lys Asp
 1 5 10 15
 Asn Phe Ile Cys Gly Cys Cys
 20

<210> 76
 <211> 293
 <212> DNA
 <213> Conus dalli

<400> 76
 caagagggat cgaatagcagt tcatgatgtc taaactggga gcctgtgtga ccatctgtct 60
 acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaactgc 120
 agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgate ccgtcaaacg 180
 gtgttgcatg gattcggaat gcaactatct ttgtctggcct tgcgtgtatt tatcataacc 240
 ttgtttatcg cggcctcatc aagtgtcaaa tgaataagta aaatgattgc agt 293

<210> 77
 <211> 71
 <212> PRT
 <213> Conus dalli

<400> 77
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
 35 40 45

Asp Pro Val Lys Arg Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50 55 60

Trp Pro Cys Cys Ile Leu Ser
65 70

<210> 78
<211> 18
<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 78
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
1 5 10 15

Leu Ser

<210> 79
<211> 299
<212> DNA
<213> Conus dalli

<400> 79
caagaggggat c gatagcagt tcatgatgtc taaactggga gtcttgttga ccatattgtct 60
acttctgttt ccccttactg ctgttccact ggatggagat cagcctgcag accgacctgc 120
agagcgtatg caggacggca tttcatctga acatcatcca ttttttgatt cgcgtaaaaa 180
gaaacaacag tggtgccgcg cggtggcatg caacatggga tgcgagcctt gttgtggatg 240
accagctttg ttatgcgcgc tcatgaagtg tcctaatgaa taagtaaaac gattgcagt 299

<210> 80
<211> 72
<212> PRT
<213> Conus dalli

<400> 80
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Phe
35 40 45

Asp Ser Val Lys Lys Lys Gln Gln Cys Cys Pro Pro Val Ala Cys Asn
50 55 60

Met Gly Cys Glu Pro Cys Cys Gly
65 70

<210> 81
<211> 17

<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 5, 6 and 15 is Pro or Hyp

<400> 81
Xaa Gln Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Xaa Xaa Cys
1 5 10 15

Cys

<210> 82
<211> 290
<212> DNA
<213> Conus dalli

<400> 82
caagaaggat cgaatagcagt tcatgatgtc taaactggga gtcttggtga tcatatgtct 60
attttctgttt ccccttactg ctgttcagct caatggagat cagcctgcag accaatctgc 120
agagcgtatg caggacaaaa ttcatctga acatcatccc ttttttgatc cgtcaaacg 180
ttgttgcaac gcgggggttt gcggttcgg atgcacgctt tgttggtgtt gaccagcttt 240
gttatcgcg cctcatcaag tgtctaatga ataagtaaaa tgattgcagt 290
<210> 83
<211> 69
<212> PRT
<213> Conus dalli

<400> 83
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Phe Leu Phe
1 5 10 15
Pro Leu Thr Ala Val Gln Leu Asn Gly Asp Gln Pro Ala Asp Gln Ser
20 25 30
Ala Glu Arg Met Gln Asp Lys Ile Ser Ser Glu His His Pro Phe Phe
35 40 45
Asp Pro Val Lys Arg Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys
50 55 60

Thr Pro Cys Cys Trp
65

<210> 84
<211> 16
<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or brom o-Tr

<400> 84
Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Xaa Cys Cys Xaa
1 5 10 15

<210> 85
 <211> 288
 <212> DNA
 <213> *Conus distans*

<400> 85
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccattcttct 60
 gctctgtgtt ccccttactg ctgttccgct ggatggagat caaccgcag acggacttgc 120
 agagcgcatg caggacgaca gttcagctgc actgattaga gactggcttc ttcaaaccog 180
 acagtgttgt gtgcatccat gcccatgcac gccttgctgt agatgaccag ctttgtcatc 240
 gcggctacgt caagtatcta atgaataagt aagtaaaacg attgcagt 288

<210> 86
 <211> 67
 <212> PRT
 <213> *Conus distans*

<400> 86
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Phe Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gly Leu
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ser Ser Ala Ala Leu Ile Arg Asp Trp
 35 40 45
 Leu Leu Gln Thr Arg Gln Cys Cys Val His Pro Cys Pro Cys Thr Pro
 50 55 60
 Cys Cys Arg
 65

<210> 87
 <211> 14
 <212> PRT
 <213> *Conus distans*

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 11 i
 s Pro or Hy

<400> 87
 Xaa Cys Cys Val His Xaa Cys Xaa Cys Thr Xaa Cys Cys Arg
 1 5 10

<210> 88
 <211> 303
 <212> DNA
 <213> *Conus ermineus*

<400> 88
 acctcaagag ggatcgatcg cagttcatga tgtctaaact gggagccttg ttgaccatct 60
 gtctgctttt gtttccatt actgctcttc tgatggatgg agatcagcct gcagaccgac 120
 ctgcagagcg tacggaggat gacatttcat ctgactacat tccctgttgc agttggccat 180

gcccccgata ctccaacggt aaacttggtt gtttttggtg ccttggtatga taatgtggtg 240
 atgaccaact ttgttatcac ggctacgtca agtgtctact gaataagtaa aatgattgca 300
 gta 303

<210> 89
 <211> 67
 <212> PRT
 <213> Conus ermineus

<400> 89
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Ile Thr Ala Leu Leu Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Thr Glu Asp Asp Ile Ser Ser Asp Tyr Ile Pro Cys Cys
 35 40 45

Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys Phe Cys
 50 55 60

Cys Leu Gly
 65

<210> 90
 <211> 20
 <212> PRT
 <213> Conus ermineus

<220>
 <221> PEPTIDE
 <222> (1)..(20)
 <223> Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue4 is Trp or
 bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 odo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 90
 Cys Cys Ser Xaa Xaa Cys Xaa Arg Xaa Ser Asn Gly Lys Leu Val Cys
 1 5 10 15

Phe Cys Cys Leu
 20

<210> 91
 <211> 241
 <212> DNA
 <213> Conus generalis

<400> 91
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttccctt 60
 actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120
 gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctgc 180
 aactttggat gccaaccttg ttgcctcacc tgataacgtg ttgatgacca actttctega 240
 g 241

<210> 92
 <211> 70
 <212> PRT

<213> *Conus generalis*

<400> 92

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys
50 55 60

Gln Pro Cys Cys Leu Thr
65 70

<210> 93

<211> 16

<212> PRT

<213> *Conus generalis*

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Pro or
Hy

<400> 93

Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Leu Thr
1 5 10 15

<210> 94

<211> 241

<212> DNA

<213> *Conus generalis*

<400> 94

ggatccatga tgtctaaact gggagtccttg ttgaccatct gtctgggtct gtttcccctt 60

actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120

gacaattcag ctgcacagaa ccctgggtt attgccatca gacagtgttg cactgtctgc 180

aactttggat gccagccttg ttgcgtcccc tgataacgtg ttgatgacca actttctcga 240

g 241

<210> 95

<211> 70

<212> PRT

<213> *Conus generalis*

<400> 95

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys

50 55 60

Gln Pro Cys Cys Val Pro
65 70

<210> 96
<211> 16
<212> PRT
<213> *Conus generalis*

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 and 16 is Pro or Hy

<400> 96
Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Val Xaa
1 5 10 15

<210> 97
<211> 862
<212> DNA
<213> *Conus geographus*

<400> 97
gtcgactcta gaggatccga caacaaagag tcaaccccac tgccacgtca agagcgaagc 60
gccacagcta agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt 120
tgaccatctg tctgcttctg tttccctcta ctgctcttcc gatggatgga gatgaacctg 180
caaaccgacc tgctegacgt atgcaggaca acatttcate tgacagtat ccttgtttg 240
agaagagacg agattgttgc actcgcgcga agaaatgcaa agaccgacaa tgcaaacccc 300
agagatgttg cgctggacga taactgtgtg atgaccaact ttatcacggc tacgtcaagt 360
gtttagttaa taagtaaaat gattgcagtc ttgtctagat ttgttttgtt gttttgtgtc 420
aaagatcaat gaccaaaccg ttgttttgat gcggattgtc atatatttct cgattccaat 480
ccaacactag atgatttaat cagcatagat taattttcta tcaatgcctt gatttttctg 540
ctgtcatatc agttttgttt atatttattt ttctgtcact gtctacacaa acgcatgcat 600
gcacgcatgc acgcacacac gcacgcacgc tcgcacaaac atgcgcgcgc acgcacacac 660
acacacacac acacaaacac acacacaagc aatcacacaa ttattgacat tatttattta 720
ttcatgtatg tatttgttat tcgtttgctt gtttttagaa tagtttgagg cgtctttttt 780
ggatttattt gaactgcttt attgtatacg agtacttcgt gctttgaaac actgctgaaa 840
ataaaacaaa cactgacgta gc 862

<210> 98
<211> 75
<212> PRT
<213> *Conus geographus*

<400> 98
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
65 70 75

<210> 99
<211> 22
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 99
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
1 5 10 15

Xaa Gln Arg Cys Cys Ala
20

<210> 100
<211> 860
<212> DNA
<213> Conus geographus

<400> 100
ggccagacga caacaaagag tcaacccccc tgccacgtca agagcgaagc gccacagcta 60
agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcctgt tgaccatctg 120
tgtgcttctg ttccccctta ctgctcttcc gatggatgga gatgaacctg caaacccgacc 180
tgtcgagcgt atgcaggaca acatttcato tgagcagtat cccttggttg agaagagagc 240
agattgtttg actccgcccga ggaaatgcaa agaccgacga tgcaaaccca tgaatgttg 300
cgctggacga taacgtgttg atgaccaact ttatcacggc tagctcagtg ttagtgaat 360
aagtaaaaatg attgcagtc tgcacagatt gcttttgtgt ttgggtctaa gatcaatgac 420
caaacccgttg ttttgatgag gattgtcata ttttctcga ttccaatcca acaatgatg 480
atttaatcac gatagattaa ttttctatca atgocctgat ttttcgtctg tcatatcagt 540
ttgttttata tttatttttt cgtcactgtc tacacaaacg catgcatgca cgcgtgcagc 600
cacacacgca cgcacgctcg cacaaacatg cgcgcgcacg cacacacaca cacacacaca 660
aacacacaca cgaagcaatc acacaattag ttgacattat ttatttatc attgatgat 720
ttgtatttcg tttgcttgtt tttagaatag tttagggcgc tctttttgga tttatttgaa 780
ctgctttatt gtatacgagt acttcgtgct ttgaaacact gctgaaaata aaacaacac 840
tgacgtagca aaaaaaaaaa 860

<210> 101
 <211> 75
 <212> PRT
 <213> Conus geographus

<400> 101
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
 20 25 30
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
 35 40 45
 Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg
 50 55 60
 Arg Cys Lys Pro Met Lys Cys Cys Ala Gly Arg
 65 70 75

<210> 102
 <211> 22
 <212> PRT
 <213> Conus geographus
 <220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 102
 Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Arg Cys Lys
 1 5 10 15
 Xaa Met Lys Cys Cys Ala
 20

<210> 103
 <211> 22
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 103
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Arg Cys Lys
 1 5 10 15
 Xaa Leu Lys Cys Cys Ala
 20

<210> 104
 <211> 321
 <212> DNA
 <213> Conus gloriamaris

<400> 104
 ctcaactatag gaattcgagc tcggtacacg ggaatcgatag cagttcatga tgtctaaact 60
 gggagccttg ttgacctct gtctacttct gttttcccta actgctgttc cgtgggatgg 120

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agatcaacat gcagaccaac ctgcagagcg tctgcatgac cgccttccaa ctgaaaatca 180
tcccttatat gatcccgta aacgggtgtg cgaatgattcg gaatgcgact attcttgctg 240
gccttgctgt atgtttggat aacctttgtt atcgcggcgt cgataagtgt ctaatgaata 300
agtaaaacga ttgcagtagg c 321

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<210> 105
<211> 71
<212> PRT
<213> Conus gloriamaris

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<400> 105
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe
1 5 10 15
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

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Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45
Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50 55 60

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Trp Pro Cys Cys Met Phe Gly
65 70

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<210> 106
<211> 17
<212> PRT
<213> Conus gloriamaris

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<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue is 6 Glu or gamma-carboxy Glu; Xaa at residue 13 i
s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
r O-phospho-Ty

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<400> 106
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
1 5 10 15

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Phe

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<210> 107
<211> 257
<212> DNA
<213> Conus gloriamaris

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<400> 107
gttcgatgatg tctaaactgg gagtcttggt gatcatctgt ctactctgt tcccccttac 60
tgctgttccg ctggatggag atcaacctgc agaccgatat gcagagcgta tgcaggacga 120
catttcatct gaacatcatc ccatgtttga tgccgtcaga ggggtgtgcc atctgttgcc 180
atgccgcttc ggaatgcctgc ctgtgtgttg gtgatcagct ttgttatcgc ggcctcatca 240
agtgactcta atgcaaaa
<210> 108
<211> 69

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<212> PRT
 <213> Conus gloriamaris

<400> 108
 Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Tyr
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Met Phe
 35 40 45
 Asp Ala Val Arg Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys
 50 55 60
 Ser Pro Cys Cys Trp
 65

<210> 109
 <211> 17
 <212> PRT
 <213> Conus gloriamaris
 <220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 17 is Trp or brom
 o-Tr

<400> 109
 Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys
 1 5 10 15
 Xaa

<210> 110
 <211> 471
 <212> DNA
 <213> Conus gloriamaris

<400> 110
 gagacgacaa ggaacagtca accccacagc cagccaaga gcagacagcc acagctacgt 60
 gaagaagggt ggagagaggt tcgtgatgtt gaaaatggga gtggtgctat tcattcttct 120
 ggtactgttt cccctggcaa cgctccagct ggatgcagat caacctgtag aacgatatgc 180
 ggagaacaaa cagctcctca acccagatga aaggaggga atcatattgc atgctctggg 240
 gacgcgatgc tgttcttggg atgtgtgcga ccaccgagt tgtacttgct gcgcgggtta 300
 gcgcggaaca tccatggcgc tgtgtgggc ggttttatcc aacaacgaca gcgtttgttg 360
 atttcagtta tcaattgcgc cagctctctt gtctaagaat gacgaacatg attgcactct 420
 ggttcagatt tcgtgttctt ttctgacaa aaatgacaaa actccaaaaa a 471

<210> 111
 <211> 71
 <212> PRT
 <213> Conus gloriamaris

<400> 111
 Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro

1 5 10 15
 Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala
 20 25 30
 Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Ile Leu
 35 40 45
 His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro
 50 55 60
 Ser Cys Thr Cys Cys Gly Gly
 65 70

<210> 112
 <211> 16
 <212> PRT
 <213> Conus gloriamaris

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo
 -Tr

<400> 112
 Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys Gly
 1 5 10 15

<210> 113
 <211> 304
 <212> DNA
 <213> Conus laterculatus

<400> 113
 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctggggagtct tgttgaccat 60
 ctgtctgctt ctgtttcccc ttactgctct tccgatggat ggagatcaac ctgcagaccg 120
 acctgcagag cgtatgcagg acgtttcctc tgaacagcat cccctgtatg atccccgtcaa 180
 acgggtgttg gactggccat gcagcgggat catcccttgt tgctaatagt aacaacgtgt 240
 tgataaccaa ctttcttacc acgactacgt caagtgtcta atgaataagt aaaatgattg 300
 cagt 304

<210> 114
 <211> 65
 <212> PRT
 <213> Conus laterculatus

<400> 114
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Val Ser Ser Glu Gln His Pro Leu Tyr Asp
 35 40 45
 Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys
 50 55 60

Cys

65

<210> 115
 <211> 13
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 5 and 11 is Pro or Hyp; Xaa at residue 4 is Trp or
 bromo-Trp

<400> 115
 Cys Cys Asp Xaa Xaa Cys Ser Gly Cys Ile Xaa Cys Cys
 1 5 10

<210> 116
 <211> 313
 <212> DNA
 <213> Conus laterculatus

<400> 116
 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagctct tgttgaccat 60
 ctgtctgctt ctgtttcccc ttactgtctt ggatggagat caacctgcag accgacttgc 120
 agagcgtatg caggacgaca ttctatctga gcagcatccc ttgaaaaga gacgagactg 180
 ttgcacacct ccgaagaaat gcagagaccg acaatgcaaa cctgcacgtt gttgcggagg 240
 ataacgtgtt gatgaccaac ttgttatca cggctacgtc aagtgtctag tgaataagta 300
 aaacgattgc agt 313

<210> 117
 <211> 71
 <212> PRT
 <213> Conus laterculatus

<400> 117
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Asp Gly Asp Gln Pro Ala Asp Arg Leu Ala Glu
 20 25 30

Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Glu Lys Arg
 35 40 45

Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys
 50 55 60

Pro Ala Arg Cys Cys Gly Gly
 65 70

<210> 118
 <211> 22
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 17 and 17 is Pro or Hyp

<400> 118

Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Arg Asp Arg Gln Cys Lys
 1 5 10 15

Xaa Ala Arg Cys Cys Gly
 20

<210> 119

<211> 314

<212> DNA

<213> Conus laterculatus

<400> 119

gggatcgata gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctgcttc 60
 tgtttccocct tactgtctctt ccgatggatg gagatcaact tgcacgccga tctgcagagc 120
 gtatgcagga caacatttca tctgagcagc atcacctctt tgaaaagaga cgaccacat 180
 gttgcaccta tgacgggagt tgcctaaaag aatcatgcat gcgtaaagct tgttgcggat 240
 gataacgtgt tgatgaccaa ctttgtttatc acggctactc aagtgtctaa tgaataagta 300
 aaatgattgc agta 314

<210> 120

<211> 74

<212> PRT

<213> Conus laterculatus

<400> 120

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Ser
 20 25 30
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His His Leu Phe
 35 40 45
 Glu Lys Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys
 50 55 60
 Glu Ser Cys Met Arg Lys Ala Cys Cys Gly
 65 70

<210> 121

<211> 22

<212> PRT

<213> Conus laterculatus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-p-sulpho-Ty

<400> 121

Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys
 1 5 10 15

Met Arg Lys Ala Cys Cys
 20

<210> 122
 <211> 314
 <212> DNA
 <213> Conus laterculatus

<400> 122
 gggatcgata gcagttcatg atgtotaaac tgggagtctt gttgaccacc tgtctgtctc 60
 tgtttccctt tactgtctct cggatggatg gagatcaact tgcacgccga cctgcagagc 120
 gttatgcagga caacatttca tctgagcagc atcccttctt tgaaaggaga cgaccaccat 180
 gttgcaccta tgacgggagt tgcctaaaag aatcatgcaa gcgtaaagct tgttgcggat 240
 aataacgtgt tgatgaccaa ctttgttato acggctactc aagtgtctaa tgaataagta 300
 aaatgattgc agta 314

<210> 123
 <211> 74
 <212> PRT
 <213> Conus laterculatus

<400> 123
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Thr Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
 35 40 45
 Glu Arg Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys
 50 55 60
 Glu Ser Cys Lys Arg Lys Ala Cys Cys Gly
 65 70

<210> 124
 <211> 22
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 (1)..(22)
 <223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 124
 Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys
 1 5 10 15
 Lys Arg Lys Ala Cys Cys
 20

<210> 125
 <211> 247
 <212> DNA
 <213> Conus leopardus

<400> 125

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ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttccccct 60
actgtctcttc ggctgggttg agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120
gacattccag atggacagca tccgttaaat gataggcaga taaactgttg cccgtggcca 180
tgccctagta catgccgcca tcaatgctgc cattaatgat aacgtgttga tgaccaactt 240
tctcgag 247

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<210> 126
<211> 71
<212> PRT
<213> Conus leopardus

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<400> 126
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
1 5 10 15
Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Gly Asp Gln Pro Ala Glu
20 25 30
Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asp Gly Gln His Pro
35 40 45
Leu Asn Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr
50 55 60
Cys Arg His Gln Cys Cys His
65 70

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<210> 127
<211> 19
<212> PRT
<213> Conus leopardus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 i
s Pro or Hyp; Xaa at residue 7 is Trp or bromo-Tr

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<400> 127
Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Ser Thr Cys Arg His Gln
1 5 10 15
Cys Cys His

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<210> 128
<211> 244
<212> DNA
<213> Conus lividus

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<400> 128
ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttccccct 60
actgtctcttc ggctgggttg agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120
gacattccaa atggacagga tccgttaatt gataggcaga taaattgttg cccttggcca 180
tgccctgatt catgccacta tcaatgctgc cactgataac gtgttgatga ccaactttct 240
cgag 244

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<210> 129

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<211> 71
 <212> PRT
 <213> *Conus lividus*

<400> 129
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Arg Asp Gln Pro Ala Glu
 20 25 30
 Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asn Gly Gln Asp Pro
 35 40 45
 Leu Ile Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser
 50 55 60
 Cys His Tyr Gln Cys Cys His
 65 70

<210> 130
 <211> 19
 <212> PRT
 <213> *Conus lividus*

<220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 is
 Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp; Xaa at residu
 e 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
 r O-phospho-Ty

<400> 130
 Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Asp Ser Cys His Xaa Gln
 1 5 10 15
 Cys Cys His

<210> 131
 <211> 275
 <212> DNA
 <213> *Conus lynceus*

<400> 131
 aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgacct ctgtctgctt 60
 ctgtttcccc ttaactgctct tccgatggat ggagatcaat ctgcagaccg acttgagag 120
 cgtatgcagg acaacatttc atctgagcag catcccttct ttgaaaagag aggacgagac 180
 tgttgcacac ctccgaggaa atgcagagac cgagcctgca aacctcaacg ttgttgcgga 240
 ggataagctg ttgatgacca actttgttat acggc 275

<210> 132
 <211> 75
 <212> PRT
 <213> *Conus lynceus*

<400> 132
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Ala Asp Arg Leu

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                20                25                30
Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
    35                40                45

Glu Lys Arg Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp
    50                55                60

Arg Ala Cys Lys Pro Gln Arg Cys Cys Gly Gly
    65                70                75

<210> 133
<211> 23
<212> PRT
<213> Conus lynceus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 7, 8 and 18 is Pro or Hyp

<400> 133
Gly Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Arg Asp Arg Ala Cys
 1          5          10         15

Lys Xaa Gln Arg Cys Cys Gly
          20

<210> 134
<211> 803
<212> DNA
<213> Conus magus

<400> 134
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga coactctgtct      60
gctttctgttt ccccttactg ctcttccgat g gatggagat gaacctgcaa accgacctgt      120
cgagcgtatg caggacaaca ttctcatctga gcagtatccc ttgtttgaga agagacgaga      180
ttgttgcaact ccgccaaga aatgcaaaga ccgacaatgc aaacccocaga gatgttgccg      240
tgagacgataa cgtgttgatg accaacttta tcacgggtac gtcaagtgtt tagtgaataa      300
gtaaaatgat tgcagtcctg ctccagatttg cttttgtggt ttggtctaaa gatcaatgac      360
caaaccgttg ttttgatgcg gattgtcata tttttctcga ttccaatcca aactagatg      420
atttaatcac gatagattaa ttttctatca atgccttgat ttttcgtctg tcatatcagt      480
tttgtttata tttatttttt cgtcactgtc tacacaaacg catgcatgca cgcgatgcacg      540
cacacacgca cgcacgctcg cacaacatg cgcgcgcacg cacacacaca cacacacaca      600
caaacacaca cacgaagcaa tcacacaatt agttgacatt atttatttat tcattgatgt      660
atttgttatt cgtttgcttg tttttagaat agtttgaggc ^gtctttttg gattttattg      720
aactgcttta ttgtatacga gtacttcgtg cggggaaaca ctgctgaaaa taaaacaaac      780
actgcgtagt caaaaaaaaa aaa                                     803

<210> 135
<211> 75
<212> PRT

```

<213> Conus magus

<400> 135

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
65 70 75

<210> 136

<211> 22

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 6 and 7 is Pro or Hyp

<400> 136

Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
1 5 10 15

Xaa Gln Arg Cys Cys Ala
20

<210> 137

<211> 656

<212> DNA

<213> Conus magus

<400> 137

caagaggggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct	60
gtctctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc	120
agatcgtatg caggacgaca ttcatctga gcagtatccc ttgtttgata tgagaaaaag	180
gtgttgccgc cccggcggtt catgccccgt atatttcaga gacaatttta ttgtgggttg	240
ttgttaaatg acaactgtgc gatgaccaac ttcattatca cgactacgcc aagtgtctaa	300
tgaataaata aaatgattgc agtotogetc agatttgott ttgtattttg gtctaaagat	360
caatgaccaa accgttgttt tgggtgggat ttcatatat ttctcagtc ctatccaaca	420
ctagatgatt taatcacgat agatctgatt tttttatcaa aggtctgggt ttctgtctgt	480
cacatcagtt ttgtttatat ttaatttttc gtcactgatt acacacacgc atgaacgcac	540
agagtactaa cacatacaca cacacacaca cacacacaca cacacacaca cacacacaca	600
cacacacaca cgcgcgcgcg cgcgcgcgcca tctagtagcg ccgcgacgac acacac	656

<210> 138

<211> 74

<212> PRT

<213> Conus magus

<400> 138

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 139

<211> 21

<212> PRT

<213> Conus magus

<220>

PEPTIDE

<222> (1)..(21)

<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue is 11 Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 139

Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe
1 5 10 15

Ile Cys Gly Cys Cys
20

<210> 140

<211> 594

<212> DNA

<213> Conus magus

<400> 140

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgttt 60
gottctgttt ccccttactg ctcttccgag ggatggagat caatctgtag accgacctgc 120
agagcgtatg caggacgaca ttcatctga gctgcatccc ttgtcaatca gaaaaagaat 180
gtgttcgggc gagagtgcgc catgccccag ctatttcaga aacagtcaga ttgttcattg 240
ttgttaaatg acaacgtgtc gatgaccacc ttcgttatca cgactaatga taagtaaaat 300
gattgcagtc tcgctcagat ttgcttttgt atttttgtct aaagatcaat gaccaaaccg 360
ttgttttgat gtggatttct atatatctct cgagtcctat ccaactatag atgatttaat 420
cacgatagat ctgatttttt tatcaaagcc ttggtttttc gtctgtcaca tcagttttgt 480
ttatatattaa tttttcgtca ctgattacac acacgcatga acgcacagac gtactaacac 540
atacacacac acacacacac acacacacac acacacacac acacacacac acac 594

<210> 141

<211> 74

<212> PRT
 <213> Conus magus

<400> 141
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Arg Asp Gly Asp Gln Ser Val Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Ser
 35 40 45
 Ile Arg Lys Arg Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr
 50 55 60
 Phe Arg Asn Ser Gln Ile Cys His Cys Cys
 65 70

<210> 142
 <211> 22
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 and
 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 142
 Met Cys Cys Gly Xaa Ser Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
 1 5 10 15
 Gln Ile Cys His Cys Cys
 20

<210> 143
 <211> 501
 <212> DNA
 <213> Conus magus

<400> 143
 caagaggggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120
 agatcgtatg caggacgaca ttcatctga gcagtatccc ttgtttgata agagacaaaa 180
 gtgttgccgc cccggcggtt catgcccggt atatttcaca gacaatttta ttgtgtgttg 240
 ttgttaaatg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300
 tgaataaata aaatgattgc agtctcgtc agatttgctt ttgtatttgg tctaaagatc 360
 aatgacaaaa ccgttgtttt ggtgtggat ttctatctat ttctcgatc ctatccaaca 420
 ctagatgatt taatcacgat agatctgatt tttttatcaa tgccctaatt ttttgcctg 480
 tcatatcagt tttgtttata t 501

<210> 144
 <211> 74
 <212> PRT

<213> Conus magus

<400> 144

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60

Phe Thr Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 145

<211> 23

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 145

Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Thr Asp
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 146

<211> 454

<212> DNA

<213> Conus magus

<400> 146

caagagggat cgaatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct	60
gtcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaactgtc	120
agatcgtatg caggacgaca ttctatctga gcagtatccc ttgtttgata agagacaaaa	180
gtgttgccgc cccggcgggt catgcccggt atatttcaga gacaatttta ttgtgtggtg	240
ttgttaaatg acaactgtgc gatgaccatc ttcatattca cgactacgcc aagtgtctaa	300
tgaataaata aaatgattgc agtctcgtc agatttgcgt ttgtattttg gtctaaagat	360
caatgaccaa accgtgtgtt tgggtgtggat ttcatatat ttctcgattc ctatccaaca	420
ctagatgatt taatcacgat agatctgatt tttt	454

<210> 147

<211> 74

<212> PRT

<213> Conus magus

<400> 147

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 148

<211> 23

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 148

Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 149

<211> 22

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 10 and 20 is
Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 149

Xaa Lys Cys Cys Ser Gly Gly Ser Cys Xaa Leu Xaa Phe Arg Asp Arg
1 5 10 15

Leu Ile Cys Xaa Cys Cys
20

<210> 150

<211> 19

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Xaa at residue 16 is Pro or Hyp

<400> 150

Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa
1 5 10 15

Cys Cys Asn

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<210> 151
<211> 321
<212> DNA
<213> Conus marmoreus
<400> 151
caagaaggat cgaatagcagt tcatgatgtc taaactggga gtcttgttga coactctgtct    60
gcttctgttt cccgttactg ctcttccgat ggaatggtgat caacctgcag accgacttgt    120
agagcgtatg caggacaaca ttctatctga gcagcatccc ttctttgaaa agagaagagg    180
aggctgttgc acacctccga ggaaatgcaa agaccgagcc tgcaaacctg cactgttgctg    240
cggcccagga taacgtgttg atgaccaact ttgttatcac ggctacgtca agtgtctagt    300
gaataagtaa aacgattgca g                                     321

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<210> 152
<211> 76
<212> PRT
<213> Conus marmoreus

<400> 152
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1          5          10
Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20         25         30
Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35         40         45
Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp
50         55         60
Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65         70         75

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<210> 153
<211> 24
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residue 3, 8, 18 and 24 is Pro or Hyp

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<400> 153
Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys
1          5          10         15
Lys Xaa Ala Arg Cys Cys Gly Xaa
20

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<210> 154
<211> 296
<212> DNA
<213> Conus marmoreus

<400> 154
gagctcggtg ccccgacctc aagagggatc gatagcagtt catgatgtct aaactgggaa    60

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tcttggtgac catctgtcta cttctatttc cccttactgc tgttccgctg gatggagatc 120
aacctgcaga cgaacctgca gagcgtatgc aggacgacat ttcattctgaa catcatccct 180
tttttgatcc cgtcaaacgg tgttgcaggt tatcatggcg cctgggatgc cacccttggt 240
gtggatgacc agctttgtta tcgcggcctc atcaagtgtc taatgaataa gtaaaa 296

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<210> 155
<211> 68
<212> PRT
<213> Conus marmoreus

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<400> 155
Met Met Ser Lys Leu Gly Ile Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Phe Phe
35 40 45
Asp Pro Val Lys Arg Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His
50 55 60
Pro Cys Cys Gly
65

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<210> 156
<211> 14
<212> PRT
<213> Conus marmoreus

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<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 12 is Pro or Hyp

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<400> 156
Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His Xaa Cys Cys
1 5 10

```

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<210> 157
<211> 355
<212> DNA
<213> Conus marmoreus

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<400> 157
ggcctacacc aagcttgcat gctgcaggt cgactctaga ggatccccga tcgatagcag 60
ttcatgatgt ctgactggg agtcttgttg accatctgtc tactctgtt tcccttact 120
gctgttcocg tggatggaga tcaacctgcg gaccgacctg cagagcgctc gcaggacgac 180
atttcatctg aacatcatcc ccattttgat tccg~gag agtggtgcgg ttcggtcgca 240
tgccgctttg gatgcgtgcc ttgttgtgta tgaccagctt tgttatcacg gcctcatcga 300
gtgtctaagt aataagtaaa acgattgcag taggcgggta ccgagctcga attcc 355

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<210> 158
<211> 69
<212> PRT

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<213> *Conus marmoreus*

<400> 158

Met Met Ser Arg Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Leu Gln Asp Asp Ile Ser Ser Glu His His Pro His Phe
35 40 45

Asp Ser Gly Arg Glu Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys
50 55 60

Val Pro Cys Cys Val
65

<210> 159

<211> 17

<212> PRT

<213> *Conus marmoreus*

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 14 i
s Pro or Hy

<400> 159

Xaa Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
1 5 10 15

Val

<210> 160

<211> 295

<212> DNA

<213> *Conus marmoreus*

<400> 160

cgacctcaag agggatcgat agcagttcat gatgtctaaa ctgggagttct tgttgaccat 60
ctgtctactt ctatttcccc ttactgctgt tccgctggat ggagaccaac ctgcagaccg 120
acctgcagag cgtatgcagg acgacatttc atctgaacgt catccttttt ttgatcgag 180
caaacagtgt tgccatctgc cggcatgccg cttcggatgt acgccttgtt gttggtgatc 240
agctttgtta tcgctctctc atcaagtgtc taatgaataa gtaaaatgat tgcag 295

<210> 161

<211> 67

<212> PRT

<213> *Conus marmoreus*

<400> 161

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Phe Phe Asp Arg
35 40 45

Ser Lys Gln Cys Cys His Leu Pro Ala Cys Arg Phe Gly Cys Thr Pro
 50 55 60

Cys Cys Trp
 65

<210> 162
 <211> 19
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residue 8 and 16 is Pro or Hyp; Xaa at residue 19 is Trp o
 r bromo-Tr

<400> 162
 Ser Lys Gln Cys Cys His Leu Xaa Ala Cys Arg Phe Gly Cys Thr Xaa
 1 5 10 15

Cys Cys Xaa

<210> 163
 <211> 235
 <212> DNA
 <213> Conus marmoreus

<400> 163
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccocctt 60
 actgctcttc cgctggatgg agatcaacct gcagaccaac gtgcagagcg tacgcaggcc 120
 gagaagcatt ccttgccctga tccgagaatg ggctgttgcc cggttccatg caaaaccagt 180
 tgcactactt tgtgttgccg gtgatgataa cgtgttgatg accaactttc tcgag 235

<210> 164
 <211> 67
 <212> PRT
 <213> Conus marmoreus

<400> 164
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Gln Arg Ala Glu Arg Thr Gln Ala Glu Lys His Ser Leu Pro Asp Pro
 35 40 45

Arg Met Gly Cys Cys Pro Phe Pro Cys Lys Thr Ser Cys Thr Thr Leu
 50 55 60

Cys Cys Gly
 65

<210> 165
 <211> 17
 <212> PRT
 <213> Conus marmoreus

<220>

<221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 5 and 7 is Pro or Hyp

<400> 165
 Met Gly Cys Cys Xaa Phe Xaa Cys Lys Thr Ser Cys Thr Thr Leu Cys
 1 5 10 15

Cys

<210> 166
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4 and 6 is Trp or bromo-Trp

<400> 166
 Cys Cys His Xaa Asn Xaa Cys Asp His Leu Cys Ser Cys Cys Gly Ser
 1 5 10 15

<210> 167
 <211> 357
 <212> DNA
 <213> Conus marmoreus

<400> 167
 gccaaagcttg catgcctgca ggatgactct agaggatccc cacctcaaga gggatcgata 60
 gcagttcatg atgtotaaac tgggagtctt gttgaccatc tgtctacttc tggttgcctt 120
 tactgctgtt ccgctggatg gagatcaacc tgcagaccga cctgcagaac gtatgcagga 180
 cgacatttca tctgaacgtc atcccatgtt tgatgccgtc agagattgtt gccgttgccc 240
 ggcatgcccc ttgtgatgca acccttggtg tggatgacca gctttgttat cgggacotca 300
 tcaagtgtct aatgaataag taaaaaacga ttcgagtggg taccgagctc gaattcc 357

<210> 168
 <211> 67
 <212> PRT
 <213> Conus marmoreus

<400> 168
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
 1 5 10 15

Ala Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Met Phe Asp Ala
 35 40 45

Val Arg Asp Cys Cys Pro Leu Pro Ala Cys Pro Phe Gly Cys Asn Pro
 50 55 60

Cys Cys Gly
 65

<210> 169
 <211> 16

<212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4, 6, 9 and 14 is Pro or Hyp

<400> 169
 Asp Cys Cys Xaa Leu Xaa Ala Cys Xaa Phe Gly Cys Asn Xaa Cys Cys
 1 5 10 15

<210> 170
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 170
 Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
 1 5 10 15

<210> 171
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 171
 Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
 1 5 10 15

<210> 172
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 172
 Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
 1 5 10 15

<210> 173
 <211> 17
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 14 is Pro or Hyp

<400> 173

Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
 1 5 10 15

Val

<210> 174
 <211> 244
 <212> DNA
 <213> Conus nobilis

<400> 174
 ggatccatga tgtctaaact gggagtcttg ttgaocatct gctacttct gtttccctt 60
 actgctcttc cgctggatga agatcaacgc gtacaccgac ctgcagagcg tatgcaggac 120
 atttcattctg atcaacatct cttctttgat ctcatcaaac ggtgctgcga gttgccatgc 180
 gggccaggct tttagctccc ttgttgctga catcaataac gtgttgatga ccaactttct 240
 cgag 244

<210> 175
 <211> 69
 <212> PRT
 <213> Conus nobilis

<400> 175
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His
 20 25 30
 Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe
 35 40 45
 Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe
 50 55 60

Cys Val Pro Cys Cys
 65

<210> 176
 <211> 15
 <212> PRT
 <213> Conus nobilis

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8
 adn 13 is Pro or Hy

<400> 176
 Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys
 1 5 10 15

<210> 177
 <211> 262
 <212> DNA
 <213> Conus nobilis

<400> 177
 ggatccatga tgtctaaact gggagtcttg ttgaocatct gctacttct gtttccctt 60

actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120
 gacatttcac ctgagcagta tcccttggtt gataagagac aaaagtgttg cactgggaag 180
 aaggggtcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240
 gttgatgacc aactttctcg ag 262

<210> 178
 <211> 78
 <212> PRT
 <213> Conus nobilis

<400> 178
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15

Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro
 35 40 45

Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys
 50 55 60

Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
 65 70 75

<210> 179
 <211> 23
 <212> PRT
 <213> Conus nobilis

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu

<400> 179
 Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
 20

<210> 180
 <211> 238
 <212> DNA
 <213> Conus pulicarius

<400> 180
 ggatccatga tgtctaaact gggagttttg ttgacctctc gctgcttctt gtttccctt 60
 actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc cttctttgat cccgtcaaac ggtgttgcaa cagctgttac 180
 atgggatgca tcccttggtg cttctagtaa taacgtgttg atgaccaact ttctcgag 238

<210> 181
 <211> 68
 <212> PRT
 <213> Conus pulicarius

<400> 181
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Phe
 35 40 45

Phe Asp Pro Val Lys Arg Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile
 50 55 60

Pro Cys Cys Phe
 65

<210> 182

<211> 14

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 182
 Cys Cys Asn Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
 1 5 10

<210> 183

<211> 238

<212> DNA

<213> Conus quercinus

<400> 183
 ggatccatga tgtctaaact gggagtottg ttgaccatct gtctgcttct gtttccctt 60
 acagctcttc agctggatgg agatcaacct gcagaccgac ctgcagagcg tacgcaggac 120
 attgcatctg aacagtatcg aaagtittgat cagagacaga ggtgttgcca gtggccatgc 180
 cccggtagtt gcagatgctg ccgtactggt taacgtgttg atgaccaact ttctcgag 238

<210> 184

<211> 70

<212> PRT

<213> Conus quercinus

<400> 184
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Arg Pro Ala Glu Arg Thr Gln Asp Ile Ala Ser Glu Gln Tyr Arg Lys
 35 40 45

Phe Asp Gln Arg Gln Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys
 50 55 60

Arg Cys Cys Arg Thr Gly
 65 70

<210> 185
 <211> 17
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr
 o or Hyp; Xaa at residue 6 is Trp or bromo-Tr

<400> 185
 Xaa Arg Cys Cys Gln Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg
 1 5 10 15

Thr

<210> 186
 <211> 15
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 186
 Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Xaa Asn
 1 5 10 15

<210> 187
 <211> 15
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 11 14 is Pro or Hyp; Xaa at residue 7 is Trp or br
 omo-Tr

<400> 187
 Cys Cys Ser Arg His Cys Xaa Val Cys Ile Xaa Cys Cys Xaa Asn
 1 5 10 15

<210> 188
 <211> 323
 <212> DNA
 <213> Conus radiatus

<400> 188
 tcaagaagga tcgatagcag ttcgatgatgt ctaaactggg agtcttgttg accatctgtc 60
 tgcttctgtt tcccttact gctcttcoga tggatggaga tcaacctgta gaccgaattg 120
 cagagcgtat gcaggacaac attcatctg agcag .aac cttctttgaa aagagactac 180
 catcgtgttg ctcccttaac ttgcggcttt gcccagtacc agcatgcaaa cgtaaccctt 240
 gttgcacagg ataactgtgt gatgaccaac tttgttatca cggctacgtc aagtgtctag 300
 tgaataagta aaacgattgc agt 323

<210> 189
 <211> 76
 <212> PRT
 <213> *Conus radiatus*

<400> 189
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Val Asp Arg Leu
 20 25 30
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Thr Phe Phe
 35 40 45
 Glu Lys Arg Leu Pro Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Pro
 50 55 60
 Val Pro Ala Cys Lys Arg Asn Pro Cys Cys Thr Gly
 65 70 75

<210> 190
 <211> 24
 <212> PRT
 <213> *Conus radiatus*

<220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residue 2, 13, 15 and 21 is Pro or Hyp

<400> 190
 Leu Xaa Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Xaa Val Xaa Ala
 1 5 10 15
 Cys Lys Arg Asn Xaa Cys Cys Thr
 20

<210> 191
 <211> 336
 <212> DNA
 <213> *Conus radiatus*

<400> 191
 aggtcgactc tagaggatcc ccaaggatcg atagcagttc atgatgtcta aactgggagt 60
 cttgttgacc atctgtctgc ttctgtttcc ccttactgct cttccgatgg atggagatca 120
 aactcgagac cgacttgcag agcgtatgca ggacgacatt tcatctgagc agcatccctt 180
 ctttaaaaag agacaacaaa gatgttgcac cgtaagagg atttgtccag taccagcatg 240
 cagaagtaaa ccttgttgca aatcataacg tattgatgac caactttgtt atcacggcta 300
 cgtcaagtgt ctagtgaata agtaaaatga ttgcag 336

<210> 192
 <211> 75
 <212> PRT
 <213> *Conus radiatus*

<400> 192
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Lys Lys Arg Gln Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Pro Val
50 55 60

Pro Ala Cys Arg Ser Lys Pro Cys Cys Lys Ser
65 70 75

<210> 193

<211> 24

<212> PRT

<213> *Conus radiatus*

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12, 14 and 20
is Pro or Hy

<400> 193

Xaa Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys
1 5 10 15

Arg Ser Lys Xaa Cys Cys Lys Ser
20

<210> 194

<211> 326

<212> DNA

<213> *Conus radiatus*

<400> 194

acctcaagaa ggatcgatag cagttcatga tgtctaaact gggagtcttg ttgaccatct 60

gtctgtctct gtttcocgtt actgctcttc cgatggatgg tgatcaacct gcagaccgac 120

ttgtagagcg tatgcaggac aacatttcac ctgagcagca tcccttcttt gaaaagagaa 180

gaggaggctg ttgcacacct ccgaggaaat gcaaagaccg agcctgcata cctgcacgtt 240

gctgcggccc aggataacgt gttgatgacc aactttgtta tcacggctac gtcaagtgtc 300

tagtgaataa gtaaaacgat tgcagt 326

<210> 195

<211> 76

<212> PRT

<213> *Conus radiatus*

<400> 195

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp
50 55 60

Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65 70 75

<210> 196
<211> 24
<212> PRT
<213> *Conus radiatus*

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

<400> 196
Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys
1 5 10 15

Lys Xaa Ala Arg Cys Cys Gly Xaa
20

<210> 197
<211> 238
<212> DNA
<213> *Conus rattus*

<400> 197
ggatccatga tgtctaaact gggagtccttg gtgaccatct gctgtcttct gttccctctt 60
gctgtctttc cactggatgg agatcaacct gcagaccacc ctgcaaagcg tacgcaagat 120
gacagttcag ctgccctgat caatgcctgg ctgatgaat cccagacttg ctgcagtaac 180
tgccgtgaag attgtgatgg ttgttgccag taacgtgttg atgaccaact tctctgag 238

<210> 198
<211> 70
<212> PRT
<213> *Conus rattus*

<400> 198
Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn
35 40 45

Ala Trp Leu Asp Glu Ser Gln Thr Cys Cys Ser Asn Cys Gly Glu Asp
50 55 60

Cys Asp Gly Cys Cys Gln
65 70

<210> 199
<211> 16
<212> PRT
<213> *Conus rattus*

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 9 is Glu or gamma-carboxy Gl

<400> 199
 Xaa Thr Cys Cys Ser Asn Cys Gly Xaa Asp Cys Asp Gly Cys Cys Gln
 1 5 10 15

 <210> 200
 <211> 327
 <212> DNA
 <213> Conus stercusmuscarum

 <400> 200
 gacctcaaga gggatcgata gcagttcgtg atgtotaaac tgggagtcctt gttgaccatc 60
 tgtctgtctt tgtttcctct tactgtctct cggatggatg gagatcaacc tgcagaccaa 120
 cctgcagatc gtatgcagga cgacatttca tctgagcagt atcccttggt tgataagaga 180
 caaaagtgtt gcaactggaa gaaggggtca tgcctcggca aagcatgcaa aaatctcaaa 240
 tgttgcctctg gacgataacg tgttgatgac caactttggt atcacggcta cgtcaagtgt 300
 ctaatgaata agtaaaacga ttgcagt 327

 <210> 201
 <211> 75
 <212> PRT
 <213> Conus stercusmuscarum

 <400> 201
 Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
 1 5 10 15

 Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala
 20 25 30

 Asp Arg Met Gln Asp Asp Ile Ser Glu Gln Tyr Pro Leu Phe Asp
 35 40 45

 Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys
 50 55 60

 Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
 65 70 75

 <210> 202
 <211> 23
 <212> PRT
 <213> Conus stercusmuscarum

 <220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu

 <400> 202
 Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15

 Lys Asn Leu Lys Cys Cys Ser
 20

 <210> 203
 <211> 316
 <212> DNA
 <213> Conus stercusmuscarum

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<400> 203
gatcgatagc agttcgtgat gtctaaactg ggagtcttgt tgaccatctg tctgcttctg      60
tttcccttta ctgctcttcc gatggatgga gatcaacctg cagaccaacc tgcagatcgt      120
atgcagaacg acatttcate tgagcagtat ccttgtttg ataagagaca aaagtgttgc      180
ggccccggcg cgtcatgccc cagatatttc aaagacaatt ttatttgtgg ttgtgtttaa      240
atgacaacgt gtcgatgacc aacttcgtta tcacgacttc gccaaagtgc taatgaataa      300
gtaaaacgat tgcagt                                     316
<210> 204
<211> 73
<212> PRT
<213> Conus stercusmuscarum

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<400> 204
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
1          5          10          15
Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala
          20          25          30
Asp Arg Met Gln Asn Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp
          35          40          45
Lys Arg Gln Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe
          50          55          60
Lys Asp Asn Phe Ile Cys Gly Cys Cys
65          70
<210> 205
<211> 23
<212> PRT
<213> Conus stercusmuscarum

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<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

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<400> 205
Xaa Lys Cys Cys Gly Xaa Gly Ala Ser Cys Xaa Arg Xaa Phe Lys Asp
1          5          10          15
Asn Phe Ile Cys Gly Cys Cys
          20
<210> 206
<211> 331
<212> DNA
<213> Conus striatus

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<400> 206
cgacctttca agagggatgc atagcagttc gcgatgtcta aactgggggt attgttgacc      60
atctgtctgc ttctgtttcc ccttactgct ctccgatgg atgaagatca acctgcagac      120
caacttgaag atcgtatgca ggacgacatt tcatctgagc agtatccctc gtttgttagg      180
agacaaaagt gttgcggcga aggtctgtca tgcccaaat atttcaaaaa caattttatt      240

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tgtggtgtgt gttaaatgac aacgtgtcga tgaccaactt cgttatcacg actacgccaa 300
gtgtcttgtc taatgataat aaaatgattc c 331

<210> 207
<211> 73
<212> PRT
<213> Conus striatus

<400> 207
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
1 5 10 15
Leu Thr Ala Leu Pro Met Asp Glu Asp Gln Pro Ala Asp Gln Leu Glu
20 25 30
Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Ser Phe Val
35 40 45
Arg Arg Gln Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe
50 55 60
Lys Asn Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 208
<211> 23
<212> PRT
<213> Conus striatus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 is Glu or g
amma-carboxy Glu; Xaa at residue 11 is Pro or Hyp; Xaa at residue
13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
O-phospho-Ty

<400> 208
Xaa Lys Cys Cys Gly Xaa Gly Ser Ser Cys Xaa Lys Xaa Phe Lys Asn
1 5 10 15
Asn Phe Ile Cys Gly Cys Cys
20

<210> 209
<211> 256
<212> DNA
<213> Conus striatus

<400> 209
ggatccatga tgtctaaact gggagtcttg ttgacogtct gtctgtctct gttccccctt 60
actgtcttc cgttggtatg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120
gacatttcat ctgacgagca tcccttggtt gataagagac aaaactgttg caatggggga 180
tgctccagca aatgggtcag agatcacgca cgttggttgcg gtcgatgata acgtgttgat 240
gaccaacttt ctgcag 256

<210> 210
<211> 75
<212> PRT

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<213> *Conus striatus*

<400> 210

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asp Glu His Pro
35 40 45

Leu Phe Asp Lys Arg Gln Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys
50 55 60

Trp Cys Arg Asp His Ala Arg Cys Cys Gly Arg
65 70 75

<210> 211

<211> 20

<212> PRT

<213> *Conus striatus*

<220>

<221> PEPTIDE

<222> (1)..(20)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Trp or
bromo-Trp

<400> 211

Xaa Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Xaa Cys Arg Asp His
1 5 10 15

Ala Arg Cys Cys
20

<210> 212

<211> 235

<212> DNA

<213> *Conus tessulatus*

<400> 212

ggatccatga tgtctaaact gggagtcctg ttgaccatgt gctgtcttct gtttcccctt 60

actgtgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taggcaggac 120

attgcaactg acgatcatcc tttgtttgat cccgtcaaac ggtgctgcc acaatgtgat 180

atgggatgca tcccttggtg catttagtaa cgtgttgatg accaaacttc tcgag 235

<210> 213

<211> 68

<212> PRT

<213> *Conus tessulatus*

<400> 213

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Met Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Arg Gln Asp Ile Ala Thr Asp Asp His Pro Leu
35 40 45

Phe Asp Pro Val Lys Arg Cys Cys His Lys Cys Tyr Met Gly Cys Ile
 50 55 60

Pro Cys Cys Ile
 65

<210> 214
 <211> 14
 <212> PRT
 <213> Conus tessulatus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 214
 Cys Cys His Lys Cys Xaa Met Gly Cys Ile Xaa Cys Cys Ile
 1 5 10

<210> 215
 <211> 238
 <212> DNA
 <213> Conus tessulatus

<400> 215
 ggatccatga tgtctaaact gggagtcttg ttgacctct gtgtgcttct gtttccctt 60
 actgctgttc cgctggatgg agatcaacct gcagaccaac ctgcagagcg tacgcagaac 120
 gagcagcatc ccttgatga tcagaaaaga aagtgttgcc ggccgccatg cgccatgagc 180
 tgccgcatgg ctagggtgtg ctattaatga taacgtgttg atgaccaact ttctcgag 238

<210> 216
 <211> 68
 <212> PRT
 <213> Conus tessulatus

<400> 216
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Val Leu
 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Gln Pro Ala Glu Arg Thr Gln Asn Glu Gln His Pro Leu Tyr Asp Gln
 35 40 45

Lys Arg Lys Cys Cys Arg Pro Cys Ala Met Ser Cys Gly Met Ala
 50 55 60

Arg Cys Cys Tyr
 65

<210> 217
 <211> 18
 <212> PRT
 <213> Conus tessulatus

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 5 and 6 is Pro or Hyp; Xaa at residue 18 is Tyr, 1

25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 217

Lys Cys Cys Arg Xaa Xaa Cys Ala Met Ser Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Xaa

<210> 218

<211> 564

<212> DNA

<213> Conus textile

<400> 218

gagtcacccc actgtcacgc caagagcggg cgccacagct aaggcaagaa ggatcgatag 60

cagttcatga tgtctaaact gggagccttg ttgaccatct gtctacttct gttttccctt 120

actgctgttc cgctggatgg agatcaacat gcagaccaac ctgcacagcg tctgcaggac 180

cgcatcccaa ctgaagatca tcccttattt gatcccaaca aacgggtgtg cccgcgggtg 240

gcatgcaaca tgggatgcaa gccttggtgt ggatgaccag ctttgtttatc gcggtctcat 300

gaagtgtcta atgaataagt aaaacgattg cagtttcgtt cagatttgct gttgtatttt 360

ggctctaaaga ttaatgacca aactgttctt ttgatccgga ttttcacgta tttctcgatt 420

cctattcaac actagataag ttaatcacga cagatctgat tttccatcaa tgccttgctt 480

tttggctctgt catataaato ttgtttatat ttaattttct gtcactttca acacgcacac 540

acacacacac acacacgcgc gcgc 564

<210> 219

<211> 69

<212> PRT

<213> Conus textile

<400> 219

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
35 40 45

Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys
50 55 60

Lys Pro Cys Cys Gly
65

<210> 220

<211> 16

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 3, 4 and 13 is Pro or Hyp

<400> 220

Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys Gly
 1 5 10 15

<210> 221

<211> 780

<212> DNA

<213> Conus textile

<400> 221

ggatccagac gacaaagaag agtcaaccca ctgccacgtc aagagcagag cccacagcta 60
 agacaagaag gatc gatagc agttcatgat gtttaaactg ggagctctgt tgaccatctg 120
 tctcctctgt ttttccctta atgctgttcc gttggatgga gatcaacctg cagaccaacc 180
 tgcagagcgt ctgctggacg acatttcatt tgaaaataat cctctttatg atcccgccaa 240
 acgggtgtgc aggacttgct tcggttgac accttggtgt ggatgaccag cctcatcaag 300
 tgtctaaca ataagtaaag cgattgcagt ctggttcaga ttacttttg tattctggtc 360
 taaagattaa tgaccaaact cttcttttga tccggatgta catatatctc togatctcta 420
 tccaacgcta gataagctaa tcacgacaga tctgattttc tgtcaatgcc ttgctttttg 480
 gtctctcata tcaactctgt ttatatattaa ttctcgtca ctatatatat atatacacac 540
 acacacacac ggaattccga ttgtccagta ccgttcttgg gatcgaggta ttgctgcgat 600
 ggcttattct gtaactctttt cttctgcgct tgatagtgat gtctctact cccatctgtg 660
 ctaccctcgg cttgatcttt gataggcgtg tgcccttcac tgggtataaa cccctctgat 720
 cctactctct ggacgcctcg ggggccaac ctccaataa agcgacatcc aatgaaaaaa 780

<210> 222

<211> 66

<212> PRT

<213> Conus textile

<400> 222

Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Asn Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Leu Asp Asp Ile Ser Phe Glu Asn Asn Pro Phe Tyr
 35 40 45

Asp Pro Ala Lys Arg Cys Cys Arg Thr Cys Phe Gly Cys Thr Pro Cys
 50 55 60

Cys Gly
 65

<210> 223

<211> 12

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> Xaa at residue 10 is Pro or Hyp

<400> 223

Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys
1 5 10

<210> 224

<211> 456

<212> DNA

<213> Conus textile

<400> 224

ggaacagtca accccacagc cagccaaga gcagacagcc acagctacgt gaagaagggt 60

ggagagaggt tcattgatgtt gaaaatggga gtggtgctat tcattcttctt ggtactgttt 120

cccctggcaa cgctccagct ggatgcagat caacctgtag aacgatatgc ggagaacaaa 180

cagctctctca acccagatga aaggaggga atcctattgc ctgctctgag gaagtctgc 240

tgtgattcga attggtgcc ctttctggat tgtgagtgt gctacggta gcgccgaaca 300

tccatggcac tgttctgggc ggtttcatcc caacaacgac agcgtttgtt gatttcatgt 360

atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tggttcagat 420

ttcgtgttct tttctgacaa taaatgacaa acctcc 456

<210> 225

<211> 70

<212> PRT

<213> Conus textile

<400> 225

Met Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe
1 5 10 15

Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr
20 25 30

Ala Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Leu
35 40 45

Leu Pro Ala Leu Arg Lys Phe Cys Cys Asp Ser Asn Trp Cys His Asp
50 55 60

Cys Glu Cys Cys Tyr Gly
65 70

<210> 226

<211> 17

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 is
s Trp or bromo-Trp; Xaa at residue 17 is Tyr, 125I-Tyr, mono-iodo
-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 226

Phe Cys Cys Asp Ser Asn Xaa Cys His Ile Ser Asp Cys Xaa Cys Cys
1 5 10 15

Xaa

<210> 227
 <211> 456
 <212> DNA
 <213> Conus textile

<220>
 <221> misc_feature
 <222> (1)..(456)
 <223> n may be any nucleotide

<400> 227
 caaggaacag tcaacccocac agccacgccca agagcagaca gccacagcta cgtgaagaag 60
 ggtggagaga ggttcgtgat gttgaaaatg ggagtgtgtc tttcatctt cctggtactg 120
 tttccctcgg caacgctcca gctggatgca gatcaacctg tagaacgata tgcggagaaac 180
 aaacagctcc tcagcccaga tgaagaggagg gaaatcatat tgcattgctct ggggacgcga 240
 tgctgttctt gggatgtgtg cgaccacccg agttgtactt gctgcggtta gcgcogaaca 300
 tccatggcgc tgtgtcgtggc ggttttatcc caacaacgac agcgtttgtt gatttcatgt 360
 atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tggttcagat 420
 ttcgtgttct tttctgacaa taaatgacaa aacncc 456

<210> 228
 <211> 70
 <212> PRT
 <213> Conus textile

<400> 228
 Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro
 1 5 10 15
 Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala
 20 25 30
 Glu Asn Lys Gln Leu Leu Ser Pro Asp Glu Arg Arg Glu Ile Ile Leu
 35 40 45
 His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro
 50 55 60
 Ser Cys Thr Cys Cys Gly
 65 70

<210> 229
 <211> 15
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo
 -Tr

<400> 229
 Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys
 1 5 10 15

<210> 230
 <211> 235
 <212> DNA
 <213> Conus textile

<400> 230
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgtcttc gttccccc 60
 actgtctctc cgctggatgg agatcaaac ccagaccaag ctgcagagcg tatgcaggcc 120
 gagcagcatc ccttgtttga tcagaaaaga cggtgtgca agtttccatg cccgcatagt 180
 tgcagatatt tgtgttgcgg gtgatgataa cgtgttgatg accaacttcc tcgag 235

<210> 231
 <211> 67
 <212> PRT
 <213> Conus textile

<400> 231
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30
 Gln Ala Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln
 35 40 45
 Lys Arg Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu
 50 55 60
 Cys Cys Gly
 65

<210> 232
 <211> 16
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 3 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 232
 Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Arg Xaa Leu Cys Cys
 1 5 10 15

<210> 233
 <211> 321
 <212> DNA
 <213> Conus tulipa

<400> 233
 cgacctcaag agggatcgat agcagttcat gtctaaactg _yagtcctgt tgacaatctg 60
 tctgtctctg ttccccccta ctgctctgcc gatggatgga gatgaacctg cagaccgacc 120
 tgcagagcgt atgcaggaca acatttcac tgagcagcat ccttggttg aggagagaca 180
 cggatgttgc aaggggcccc aaggatgctc ctccagagaa tgcagacccc aacattgttg 240

cggtcgacga taacgtgttg agggccaact ttgttatcac ggctacgtca agtgtttagt 300
gaataagtaa aatgattgca g 321

<210> 234
<211> 74
<212> PRT
<213> Conus tulipa

<400> 234
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
1 5 10 15
Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asp Arg Pro Ala
20 25 30
Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Leu Phe Glu
35 40 45
Glu Arg His Gly Cys Cys Lys Gly Pro Glu Gly Cys Ser Ser Arg Glu
50 55 60

Cys Arg Pro Gln His Cys Cys Gly Arg Arg
65 70

<210> 235
<211> 21
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> Xaa at residue 8 and 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 and 17 is Pro or Hy

<400> 235
His Gly Cys Cys Lys Gly Xaa Xaa Gly Cys Ser Ser Arg Xaa Cys Arg
1 5 10 15
Xaa Gln His Cys Cys
20

<210> 236
<211> 287
<212> DNA
<213> Conus figulinus

<400> 236
caagaaggat cgaatagcagt tcatgatgtc taaactggga gtcttgctga ccactgtgtc 60
gcttctgatt ccccttactg ctcttttcgct ggatggagat caacctgcag accgacctgc 120
agagcgtatg caggatggaa ttcatctga acagcatccc atgtttgatc ccgtcagacg 180
gtgttgcccg tggccatgca acataggatg cgtaccttgt tgttgatgac cagttttgtt 240
atcgcgccct catcaaatgt ctaatgaata agtaaaacga ttgcagt 287

<210> 237
<211> 67
<212> PRT
<213> Conus figulinus

<400> 237

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Ile
1 5 10 15

Pro Leu Thr Ala Leu Ser Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu Gln His Pro Met Phe
35 40 45

Asp Pro Val Arg Arg Cys Cys Pro Trp Pro Cys Asn Ile Gly Cys Val
50 55 60

Pro Cys Cys
65

<210> 238

<211> 14

<212> PRT

<213> Conus figulinus

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 3, 5 and 12 is Pro or Hyp; Xaa at residue 4 is Trp
or bromo-Tr

<400> 238

Cys Cys Xaa Xaa Xaa Cys Asn Ile Gly Cys Val Xaa Cys Cys
1 5 10

<210> 239

<211> 283

<212> DNA

<213> Conus figulinus

<400> 239

caagagggat cgaatagcagt tcatgatgtt taaactggga gtccgtgtga ccattctgtat 60

gtttctgttt ccccttactg ctcttccgct ggatggagag caacctgcag accaacctgc 120

agagcgcatg cagtatgaca tgttacgtgc aatgaatccc tggtttgatc ccgtcaaaaag 180

gtgtgtgtcg aagaactgcg cagtatgcat cccttggtgc ccgtaactga ccagcttgat 240

tatcgcggcc aaggctctaa tgaataagta aaacgattgc agt 283

<210> 240

<211> 67

<212> PRT

<213> Conus figulinus

<400> 240

Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu Leu Phe
1 5 10 15

Pro Phe Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Met Asn Pro Trp Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro
50 55 60

Cys Cys Pro

65

<210> 241
 <211> 14
 <212> PRT
 <213> Conus figulinus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 241
 Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa
 1 5 10

<210> 242
 <211> 286
 <212> DNA
 <213> Conus figulinus

<400> 242
 caagagggat cgaatagcagt tcatgatgtc taaactgaga gctttgttga ccttatgtct 60
 gctttctgttt ccccttactg ctcttcgcgt gaatgaagat caacctgcag agcgatgca 120
 ggacgacaat tcatctgagc agcaccocct gtatgaccac aaacgaaagt gttgccggtg 180
 gccatgcccc gcaagatgcg gctcttgggt cctgtaataa cgtgttgccc aactttgtta 240
 tcacggccac gtcaaatgtt taatgaataa gtaaacgat tgcagt 286

<210> 243
 <211> 64
 <212> PRT
 <213> Conus figulinus

<400> 243
 Met Met Ser Lys Leu Arg Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Leu Asn Glu Asp Gln Pro Ala Glu Arg Met
 20 25 30
 Gln Asp Asp Asn Ser Ser Glu Gln His Pro Leu Tyr Asp His Lys Arg
 35 40 45
 Lys Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu
 50 55 60

<210> 244
 <211> 15
 <212> PRT
 <213> Conus figulinus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp

<400> 244
 Cys Cys Arg Xaa Xaa Cys Xaa Ala Arg Cys Gly Ser Cys Cys Leu
 1 5 10 15

<210> 245

<211> 301
 <212> DNA
 <213> *Conus figulinus*

<400> 245
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccttatgtct 60
 gcttctgttt cccctgactg ctcttccgct ggatgaagat caagctgcag accgacctgc 120
 agagcgtatg cagggcgatg catctgaaca gcateccttc ttgatcccg tcaaacggtg 180
 ttgcgagttg tcacgctgcc ttggatgcgt ccttggttgc acatcttaat aacgtgtgga 240
 tgaccaactg tgttatcacg gccacgtcaa gtgtctaata aataagtaaa atgattgcag 300
 t 301

<210> 246
 <211> 68
 <212> PRT
 <213> *Conus figulinus*

<400> 246
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Ala Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Gly Met Ser Glu Gln His Pro Phe Phe Asp
 35 40 45
 Pro Val Lys Arg Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro
 50 55 60
 Cys Cys Thr Ser
 65

<210> 247
 <211> 16
 <212> PRT
 <213> *Conus figulinus*

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 3 and 12 is Pro or Hyp

<400> 247
 Cys Cys Xaa Leu Ser Arg Cys Leu Gly Cys Val Xaa Cys Cys Thr Ser
 1 5 10 15

<210> 248
 <211> 301
 <212> DNA
 <213> *Conus figulinus*

<400> 248
 caagagggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccttatgtct 60
 gcttctgttt cccctgactg ctcttccgct ggatgaagat caacctgcag accgacctgc 120
 agagcgtatg cagggcgatg catctgaaca gcateccttc ttgatcccg tcaaacggtg 180
 ttgcgagttg tcaaaaatgcc atggatgcgt ccttggttgc ataccttaat aacgtgcgga 240

tgaccaactg tggttatcacg gccacgtcaa gtgtctaatag aataagtaaa atgattgcag 300

t 301

<210> 249
<211> 68
<212> PRT
<213> Conus figulinus

<400> 249
Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro
50 55 60

Cys Cys Ile Pro
65

<210> 250
<211> 16
<212> PRT
<213> Conus figulinus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 12 a
nd 16 is Pro or Hy

<400> 250
Cys Cys Xaa Leu Ser Lys Cys His Gly Cys Val Xaa Cys Cys Ile Xaa
1 5 10 15

<210> 251
<211> 298
<212> DNA
<213> Conus quercinus

<400> 251
caagagggat cgatagcagt tcatgatgtc taaactcgga gtcttgttga ccatctgtct 60

ggttctgttt cccottacag ctcttcagct ggaaggagat caacctgcag acogacctgc 120

agagcgtaag caggacattt catctgaaca gtatcgaaag ttgatcaga gacagaggtg 180

ttgccggtgg ccatgccccc gtagtgcag atgctgccgt tatcgtaaac gtgttggtga 240

ccagttttgt tatcacgacc acgccaaagt tctaacgaat aagtaaaatg attgcagt 298

<210> 252
<211> 68
<212> PRT
<213> Conus quercinus

<400> 252
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro

20 25 30
 Ala Glu Arg Thr Gln Asp Ile Ser Ser Glu Gln Tyr Arg Lys Phe Asp
 35 40 45

Gln Arg Gln Arg Cys Cys Arg Trp Pro Cys Pro Gly Ser Cys Arg Cys
 50 55 60

Cys Arg Tyr Arg
 65

<210> 253
 <211> 18
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr
 o or Hyp; Xaa at residue 6 is Trp or bromo-Trp; Xaa at residue 17
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
 phospho-Ty

<400> 253
 Xaa Arg Cys Cys Arg Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg
 1 5 10 15

Xaa Arg

<210> 254
 <211> 313
 <212> DNA
 <213> Conus quercinus

<400> 254
 caagagggat cgaatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60
 gcttctgttt ccccttactg ctcttcact ggatggagat caacctgcag atcaatctgc 120
 agagcgacct gcagagcgta cgcaggacga cattcagcag catccgttat atgatccgaa 180
 aagaaggtgt tgccgttato catgcccca cagctgccac ggatcttgcgt gctataagtg 240
 ataacatggt gatggccagc tttgttatca cggccacgtc aagtgtctaa tgaataagta 300
 aaacgattgc agt 313

<210> 255
 <211> 72
 <212> PRT
 <213> Conus quercinus

<400> 255
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ser
 20 25 30

Ala Glu Arg Pro Ala Glu Arg Thr Gln Asp Asp Ile Gln Gln His Pro
 35 40 45

Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser
 50 55 60

Cys His Gly Ser Cys Cys Tyr Lys
65 70

<210> 256
<211> 18
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 and 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 256
Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys
1 5 10 15

Xaa Lys

<210> 257
<211> 256
<212> DNA
<213> Conus wittigi

<400> 257
ggatccatga tgtctaaact gggagtccttg ttgaccatct gtctgtctct gtttccatt 60
actgctcttc cgggtgggtgg agatcagcct gcagaccgac ttgcagagcg tatgcaggac 120
gacacttcat ctgagcagca tccctttgaa aagagactac catcatgttg cgactttgag 180
aggtttgctg tagtaccagc atgcatacgt catcagtgtt gcacaggata acgtgttgat 240
gaccaacttt ctcgag 256

<210> 258
<211> 74
<212> PRT
<213> Conus wittigi

<400> 258
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15
Pro Ile Thr Ala Leu Pro Val Gly Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30
Ala Glu Arg Met Gln Asp Asp Thr Ser Ser Glu Gln His Pro Phe Glu
35 40 45
Lys Arg Leu Pro Ser Cys Cys Asp Phe Glu Arg Leu Cys Val Val Pro
50 55 60

Ala Cys Ile Arg His Gln Cys Cys Thr Gl
65 70

<210> 259
<211> 23
<212> PRT
<213> Conus wittigi

<220>

<221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 8 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 14 is Pro or Hy

<400> 259
 Leu Xaa Ser Cys Cys Asp Phe Xaa Arg Leu Cys Val Val Xaa Ala Cys
 1 5 10 15
 Ile Arg His Gln Cys Cys Thr
 20

<210> 260
 <211> 14
 <212> PRT
 <213> Conus betulinus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 14 is Trp or brom o-Tr

<400> 260
 Cys Cys Lys Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys Xaa
 1 5 10

<210> 261
 <211> 259
 <212> DNA
 <213> Conus tulipa

<220>
 <221> misc_feature
 <222> (1)..(259)
 <223> n may be any nucleotide

<400> 261
 ggtccatga tgtctaaact gggagtcttg ttgacaatct gctgcttct gtttccoctt 60
 actgctctgc cgatggatgg agatgaacct gcagaccgac ctgcagagcg tatgcaggac 120
 aacatttcatt ctgagcagca tccttctgtt gaggagagac acggatgttg cgagggggccg 180
 aagggatgct cctccagaga atgcagaccc caacattggt gcggatcgacg ataacgtgtt 240
 gatgaccaac tntctcgag 259

<210> 262
 <211> 75
 <212> PRT
 <213> Conus tulipa

<400> 262
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Leu Phe
 35 40 45
 Glu Glu Arg His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg
 50 55 60

Glu Cys Arg Pro Gln His Cys Cys Gly Arg Arg
65 70 75

<210> 263
<211> 21
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> Xaa at residue 5 and 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 and 17 is Pro or Hy

<400> 263
His Gly Cys Cys Xaa Gly Xaa Lys Gly Cys Ser Ser Arg Xaa Cys Arg
1 5 10 15

Xaa Gln His Cys Cys
20

<210> 264
<211> 262
<212> DNA
<213> Conus aurisiacus

<220>
<221> misc_feature
<222> (1)..(262)
<223> n may be any nucleotide

<400> 264
ggatccatga tgtctaaact gggagtccttg ttgaccatct gtctactttct gtttccccctt 60
actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120
gacattttcat ctgagcagta tcccttgttt gataagagac aaaagtgttg cactgggagg 180
aagggtcat gtcctggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240
gttgatgacc aactttctcg an 262

<210> 265
<211> 76
<212> PRT
<213> Conus aurisiacus

<400> 265
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Lys Arg Gln Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly
50 55 60

Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
65 70 75

<210> 266

<211> 23
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu

<400> 266
 Xaa Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
 20

<210> 267
 <211> 239
 <212> DNA
 <213> Conus betulinus

<400> 267
 ggatccatga tgtctaaact gggagtcttg ttgacctct gtctgcttct gtttcccctt 60
 actgctgttgc cgttggtgag agatcaacct gcagaccaac ctgcagagcg tatgcagaac 120
 gagcagcatc cctcgtttga tcagaaaaga aggtgctgcc ggtggccatg ccccgatata 180
 tgcggcatgg etaggtgttg cttcgtcatg ataactgtgt gatgaccaac tttctcgag 239

<210> 268
 <211> 71
 <212> PRT
 <213> Conus betulinus

<400> 268
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Met Gln Asn Glu Gln His Pro Ser Phe Asp Gln Lys Arg
 35 40 45

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
 50 55 60

Cys Phe Val Met Ile Thr Cys
 65 70

<210> 269
 <211> 23
 <212> PRT
 <213> Conus betulinus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or
 bromo-Tr

<400> 269
 Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Phe Val Met Ile Thr Cys
20

<210> 270
<211> 226
<212> DNA
<213> Conus betulinus

<220>
<221> misc_feature
<222> (1)..(226)
<223> n may be any nucleotide

<400> 270
ggatccatga tgtctaaact gggagtcttg ttgatcatct gtctgcttct gttccocctt 60
actgctgttc cgctgtagtg agatcagcct gcagagcgta cgcagatcga gcagcatccc 120
ttgtttgacc agaaaagaag gtgttgccgg tggccatgcc ccagtagatg cggcattggct 180
agggtgttgct tcgtcatgat aacgtgttga tganegacct ctcnag 226

<210> 271
<211> 67
<212> PRT
<213> Conus betulinus

<400> 271
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Phe
1 5 10 15
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Glu Arg Thr
20 25 30
Gln Ile Glu Gln His Pro Leu Phe Asp Gln Lys Arg Arg Cys Cys Arg
35 40 45
Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys Cys Phe Val Met
50 55 60

Ile Thr Cys
65

<210> 272
<211> 23
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or
bromo-Tr

<400> 272
Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser A-- Cys Gly Met Ala Arg Cys
1 5 10 15
Cys Phe Val Met Ile Thr Cys
20

<210> 273
<211> 262
<212> DNA
<213> Conus parius

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<400> 273
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccctt      60
actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatgcaggac      120
aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggaggctg ttgcacacct      180
ccgaagaaat gcaaagaccg agcctgcaaa cctgcacgtt gctgcggccc aggataacct      240
gttgatgacc aactttctcg cc                                             262

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<210> 274
<211> 76
<212> PRT
<213> Conus parius

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<400> 274
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1          5          10          15
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
          20          25          30
Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
          35          40          45
Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp
          50          55          60
Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
          65          70          75

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<210> 275
<211> 24
<212> PRT
<213> Conus parius

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<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

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<400> 275
Arg Gly Gly Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Ala Cys
1          5          10          15
Lys Xaa Ala Arg Cys Cys Gly Xaa
          20

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<210> 276
<211> 259
<212> DNA
<213> Conus parius
<400> 276
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccctt      60
actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatgcaggac      120
aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggtgtgtt cacacctccg      180
aggaaatgca aagaccgagc ctgcaaacct gcacgttgtt gcggcccagg ataacgtgtt      240
gatgaccaac tttctcgag                                             259

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<210> 277
 <211> 75
 <212> PRT
 <213> Conus parius

<400> 277
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
 20 25 30
 Val Glu Arg Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
 35 40 45
 Glu Lys Arg Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg
 50 55 60
 Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
 65 70 75

<210> 278
 <211> 23
 <212> PRT
 <213> Conus parius
 <220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

<400> 278
 Arg Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys
 1 5 10 15
 Xaa Ala Arg Cys Cys Gly Xaa
 20

<210> 279
 <211> 241
 <212> DNA
 <213> Conus coronatus

<400> 279
 ggatccatga tgtctaaact gggagtcttg ttgacctct gtctgcttct gtttccaatt 60
 actgcccttc cgctggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc ctgttttgat ccggtcaaac ggtgctgcga ttggccatgc 180
 atoccaggat gcaccctctg ttgcttgcc tgcataacgtg ttgatgacca actttctcga 240
 g 241

<210> 280
 <211> 68
 <212> PRT
 <213> Conus coronatus

<400> 280
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
 1 5 10 15
 Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
 35 40 45

Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ile Pro Gly Cys Thr Pro
 50 55 60

Cys Cys Leu Pro
 65

<210> 281
 <211> 16
 <212> PRT
 <213> Conus coronatus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 5, 8, 12 and 16 is Pro or Hyp; Xaa at residue 4 is
 Trp or bromo-Tr

<400> 281
 Cys Cys Asp Xaa Xaa Cys Ile Xaa Gly Cys Thr Xaa Cys Cys Leu Xaa
 1 5 10 15

<210> 282
 <211> 244
 <212> DNA
 <213> Conus musicus

<400> 282
 ggatccatga tgtctaaact gggagtcctg ttgacctct gtctgcttct gtttctctt 60
 tetgtctctt cgaatgatga agatcaactt gcagacctac ctgcagagcg tatgcgggac 120
 actgcaactg tagatcatcc ctctatgat cctgacaaaag cgtgctgcga gcagagctgt 180
 acaacatgct ttccgtgctg ctgacctga acacagtaac gtgttgatga ccaactttct 240
 cgag 244

<210> 283
 <211> 65
 <212> PRT
 <213> Conus musicus

<400> 283
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Ser Ala Leu Pro Met Asp Glu Asp Gln Leu Ala Asp Leu Pro
 20 25 30

Ala Glu Arg Met Arg Asp Thr Ala Thr Val Asp His Pro Ser Tyr Asp
 35 40 45

Pro Asp Lys Ala Cys Cys Glu Gln Ser Cys Thr Thr Cys Phe Pro Cys
 50 55 60

Cys
 65

<210> 284
 <211> 14
 <212> PRT

<213> *Conus musicus*

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 4 is Glu or gamma-carboxy Glu; Xaa at residue 12 is Pro or Hy

<400> 284

Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Phe Xaa Cys Cys
1 5 10

<210> 285

<211> 14

<212> PRT

<213> *Conus betulinus*

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 4 is Glu or gamma-carboxy Glu; Xaa at residue 12 is Pro or Hy

<400> 285

Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys
1 5 10

<210> 286

<211> 14

<212> PRT

<213> *Conus betulinus*

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 11 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Tr

<400> 286

Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys Xaa
1 5 10

<210> 287

<211> 235

<212> DNA

<213> *Conus pennaceus*

<400> 287

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccccc 60
actgtctcttc cgctggatgg agatcaaacct gcataccaag ctgcagagcg tatgcaggcc 120
gagcatcatc ccttgtttga tcagaaaaga cgggtgtgca agtttccatg cccgatagt 180
tgcaaatatt tgtgttgagg gtgatgataa catgttgatg accaactttc ttgag 235

<210> 288

<211> 65

<212> PRT

<213> *Conus pennaceus*

<400> 288

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Tyr Gln Ala
20 25 30

Ala Glu Arg Met Gln Ala Glu His His Pro Leu Phe Asp Gln Lys Arg
35 40 45

Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys
50 55 60

Gly
65

<210> 289

<211> 16

<212> PRT

<213> *Conus pennaceus*

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 289

Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Lys Xaa Leu Cys Cys
1 5 10 15

<210> 290

<211> 241

<212> DNA

<213> *Conus pulicarius*

<400> 290

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtetgcttct gtttccctt 60
actgctcttc cgatggatgg tgatcaactt gcagaccgac ttgtagagcg tatgcaggac 120
aacatttcat ctgagcagca tcccttcttt gatcccgta aacgggtgtt cgtcagctgt 180
tatatgggat gcatecccttg ttgcttctag taataacgtg ttgatgacca actttctoga 240
g 241

<210> 291

<211> 67

<212> PRT

<213> *Conus pulicarius*

<400> 291

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Asp Arg Leu
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro
50 55 60

Cys Cys Phe
65

<210> 292
 <211> 14
 <212> PRT
 <213> Conus pulicarius

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 292
 Cys Cys Val Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
 1 5 10

<210> 293
 <211> 244
 <212> DNA
 <213> Conus pulicarius

<400> 293
 ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtgtccccc 60
 actgctcttc cactggatga agatcaactt gcagaccgac ctgcagagcg tatgcaggat 120
 gacacttcag ctgcacagat tttcgggttt gatcccgta aacggtgctg caaattgcta 180
 tgctactcgg gatgcactcc ttgttgccat attgataac gtgttgatga ccaactttct 240
 cgag 244

<210> 294
 <211> 67
 <212> PRT
 <213> Conus pulicarius

<400> 294
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Cys
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Leu Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Thr Ser Ala Ala Gln Ile Phe Gly Phe
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys
 50 55 60

Cys His Ile
 65

<210> 295
 <211> 16
 <212> PRT
 <213> Conus pulicarius

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 295
 Cys Cys Lys Leu Leu Cys Xaa Ser Gly Cys Thr Xaa Cys Cys His Ile

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1              5              10              15

<210> 296
<211> 259
<212> DNA
<213> Conus rattus

<400> 296
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttgt gtttcogctt      60
actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatacaggac      120
aacatttcac ctgagcagca tcccttcttt gaaaagagaa gaggtgtgtg cgcacctccg      180
aggaaatgca aagaccgagc ctgcaaacct gcaogttgct ggggccaggg ataacgtgtt      240
gatgaccaac tttctogag                                     259

<210> 297
<211> 75
<212> PRT
<213> Conus rattus

<400> 297
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Val Phe
1              5              10              15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20              25              30

Val Glu Arg Ile Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35              40              45

Glu Lys Arg Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg
50              55              60

Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65              70              75

<210> 298
<211> 23
<212> PRT
<213> Conus rattus

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

<400> 298
Arg Gly Cys Cys Ala Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys
1              5              10              15

Xaa Ala Arg Cys Cys Gly Xaa
20

<210> 299
<211> 262
<212> DNA
<213> Conus stercusmuscarum

<400> 299
ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gtttcocctt      60
attgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac      120

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gacatttcat ctgagaagca tcccttgttt gataagagac aacggtgttg caatgggcgg 180
 aggggatgct ccagcagatg gtgcagagat cactcacgtt gttgcggtcg acgataacgt 240
 gttgatgacc aactttctcg ag 262
 <210> 300
 <211> 76
 <212> PRT
 <213> Conus stercusmuscarum
 <400> 300
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Ile Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Lys His Pro Leu Phe
 35 40 45
 Asp Lys Arg Gln Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg
 50 55 60
 Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
 65 70 75
 <210> 301
 <211> 22
 <212> PRT
 <213> Conus stercusmuscarum
 <220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Trp or
 bromo-Tr
 <400> 301
 Xaa Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Xaa Cys Arg
 1 5 10 15
 Asp His Ser Arg Cys Cys
 20
 <210> 302
 <211> 241
 <212> DNA
 <213> Conus ebraceus
 <400> 302
 ggatccatga tgtctaaact gggagtcttg ttgacctct gtctgtctct gtttccctt 60
 actgtctctt cactggatga aggtcaacct gcagacctac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc cttgtttgat cctgtcaaac ggtgttgcca gcagccatgc 180
 tacatgggat gcattccctt ttgtttctaa taataacgtg ttgatgacca actttctcga 240
 g 241
 <210> 303
 <211> 67
 <212> PRT

<213> Conus ebraceus

<400> 303

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Gly Gln Pro Ala Asp Leu Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro
50 55 60

Cys Cys Phe
65

<210> 304

<211> 15

<212> PRT

<213> Conus ebraceus

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 304

Cys Cys Xaa Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10 15

<210> 305

<211> 241

<212> DNA

<213> Conus ebraceus

<400> 305

ggatccatga tgtctaaact gggagtcttg ttgacctct gtctgcttct gtttcccctt 60

actgtctttc cactggatga agatcaacct gcagacctac ctgcagagcg tatgcaggac 120

attgcaactg aacagcatcc cttgtttgat cctgtcaaac ggtgctgcgc gcagccatgc 180

tacatgggat gcatcccttg ttgcttctaa taataacgtg ttgatgacca actttctoga 240

g 241

<210> 306

<211> 67

<212> PRT

<213> Conus ebraceus

<400> 306

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Leu Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro

50

55

60

Cys Cys Phe
65

<210> 307
<211> 15
<212> PRT
<213> Conus ebraceus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 307
Cys Cys Ala Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10 15

<210> 308
<211> 238
<212> DNA
<213> Conus flavidus

<400> 308
ggatccatga tgtctaaaact gggagtctgtg ttgacctct gtctgcttct gtttcccctt 60
actgctgttc cgttggtatgg agatcaacct gcagaccagc ctgcagagcg tatgcagaac 120
gagcagcatc ccttggttga tcagaaaaga aggtgctgcc ggtggccatg cccagcata 180
tgcggcatgg ctagggtgtg ctgctcatga taacgtgttg atgaccaact ttctcgag 238

<210> 309
<211> 67
<212> PRT
<213> Conus flavidus

<400> 309
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Met Gln Asn Glu Gln His Pro Leu Phe Asp Gln Lys Arg
35 40 45

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
50 55 60

Cys Ser Ser
65

<210> 310
<211> 19
<212> PRT
<213> Conus flavidus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or

bromo-Tr

<400> 310
 Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Ser Ser

<210> 311
 <211> 245
 <212> DNA
 <213> Conus miliaris

<220>
 <221> misc_feature
 <222> (1)..(245)
 <223> n may be any nucleotide

<400> 311
 ggatccatga tgtctaaact gggagtccttg ttgaccatct gctgcttct gtttccaatt 60
 actgcccttc cactggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc ctgttttgat cccgtcaaac ggtgttgcca ttggccatgc 180
 agcgcaggat gctacccttg ttgcttccct taataacgtg ttgatgacca actnangnaa 240
 aaaaaa 245

<210> 312
 <211> 68
 <212> PRT
 <213> Conus miliaris

<400> 312
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
 35 40 45

Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro
 50 55 60

Cys Cys Phe Pro
 65

<210> 313
 <211> 16
 <212> PRT
 <213> Conus miliaris

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 5, 12 and 16 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp; Xaa at residue 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 313
 Cys Cys Asp Xaa Xaa Cys Ser Ala Gly Cys Xaa Xaa Cys Cys Phe Xaa
 1 5 10 15

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<210> 314
<211> 230
<212> DNA
<213> Conus miliaris

<220>
<221> misc_feature
<222> (1)..(230)
<223> n may be any nucleotide
<400> 314
ggatccatga tgtctaaact gggagtgtgtg ccattcgtct ttctgggtct gtttcccttg      60
gcaacactcc aactggatgc agatcaacct gcagaccgac ctgcgcgtaa aaagggcatt      120
gcaactaac ggcaccctt gtctgatect gtcagagggt gttgccctcc aatgtgcaca      180
ccatgcttcc cttgctgttt tcgttaataa cgtgttgatg natgatgnan      230

<210> 315
<211> 66
<212> PRT
<213> Conus miliaris

<400> 315
Met Met Ser Lys Leu Gly Val Val Pro Phe Val Phe Leu Val Leu Phe
1          5          10          15
Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Ala Asp Arg Pro
20          25          30
Ala Arg Lys Lys Gly Ile Ala Thr Lys Arg His Pro Leu Ser Asp Pro
35          40          45
Val Arg Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys
50          55          60
Phe Arg
65

<210> 316
<211> 16
<212> PRT
<213> Conus miliaris

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 4, 9 and 12 is Pro or Hyp; Xaa at residue 5 is Tyr
      , 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
      -Ty

<400> 316
Gly Cys Cys Xaa Xaa Met Cys Thr Xaa Cys Phe Xaa Cys Cys Phe Arg
1          5          10          15

<210> 317
<211> 295
<212> DNA
<213> Conus ammiralis

<400> 317
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccattcgtct      60
gtcttcgttt cccttactg ctcttcgct ggatggagat caacctgcag accaagctgc      120

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agagcgtatg caggccgagc agcatccctt gttgatcag aaaagacggt gttgcaggtt 180
 tccatgcccc gatacttgca gacatttggt ttgcgggtga tgataacgtg ctgatgacct 240
 actttgtcat cacggctacg tcaagtgtct aatgaata; taaaatgatt gcagt 295
 <210> 318
 <211> 65
 <212> PRT
 <213> Conus ammiralis

 <400> 318
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ala
 20 25 30
 Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln Lys Arg
 35 40 45
 Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys
 50 55 60
 Gly
 65
 <210> 319
 <211> 16
 <212> PRT
 <213> Conus ammiralis

 <220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 6 and 8 is Pro or Hyp

 <400> 319
 Arg Cys Cys Arg Phe Xaa Cys Xaa Asp Thr Cys Arg His Leu Cys Cys
 1 5 10 15
 <210> 320
 <211> 267
 <212> DNA
 <213> Conus ammiralis

 <400> 320
 caagagggat cgatagcagt tcatgatgtt taaactggga gtcttgtctga coactctgtct 60
 acttctgttt tcccttaaatg ctgttccgct ggatggagat caacctgcag accaacctgc 120
 agagcgtctg ctggacgaca ttcatctga aaataatccc ttttatgatc ccgccaacag 180
 gtgttgcatg acttgctctg gttgcacacc ttgttggtga tgaccagcct catcaagtgt 240
 ctaacgaata agtaaaacga ttgcagt 267
 <210> 321
 <211> 66
 <212> PRT
 <213> Conus ammiralis

 <400> 321
 Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Asn Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Leu Asp Asp Ile Ser Ser Glu Asn Asn Pro Phe Tyr
35 40 45

Asp Pro Ala Lys Arg Cys Cys Met Thr Cys Phe Gly Cys Thr Pro Cys
50 55 60

Cys Gly
65

<210> 322
<211> 12
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(12)
<223> Xaa at residue 10 is Pro or Hyp

<400> 322
Cys Cys Met Thr Cys Phe Gly Cys Thr Xaa Cys Cys
1 5 10

<210> 323
<211> 294
<212> DNA
<213> Conus ammiralis

<400> 323
caagaaggat cgatagcagt toatgatgtc taaactggga gcccttgtga ccatctgtct 60
acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacctgc 120
agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgacg cgtcaaacg 180
gtgttcgat gattcggaat gcgactattc ttgctggcct tgctgtattt tttcataacc 240
tttgttatcg cggcctcatc ctagtgtcaa atgaataagt aaaacgattg cagt 294

<210> 324
<211> 71
<212> PRT
<213> Conus ammiralis

<400> 324
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50 55 60

Trp Pro Cys Cys Ile Phe Ser
65 70
<210> 325
<211> 18

<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 325
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
1 5 10 15

Phe Ser

<210> 326
<211> 284
<212> DNA
<213> Conus ammiralis

<400> 326
caagagggat cgatagcagt tcatgatgtt taaactcgga gtcttgcgtg ccatctgtct 60
acttctgttt tccctaattg ctgttccgct ggatggagat caacatgcag accaacctgc 120
agagcgtctg caggacogcc ttccaactga aaatcatccc ttatatgato ccgtcaaacg 180
gtgttgacagg ttgttatgcc tcagttgcaa ccctgttgtt ggatgaccag ctttgtttac 240
acggcctcat caagtgtcta atgaataagt aaaacgattg cagt 284

<210> 327
<211> 67
<212> PRT
<213> Conus ammiralis

<400> 327
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
1 5 10 15

Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45

Asp Pro Val Lys Arg Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Pro
50 55 60

Cys Cys Gly
65

<210> 328
<211> 13
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(13)
<223> Xaa at residue 11 is Pro or Hyp

<400> 328

Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Xaa Cys Cys
1 5 10

<210> 329
<211> 289
<212> DNA
<213> Conus ammiralis

<400> 329
caagaaggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccattctgtct 60
acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaactctgc 120
agagcgtctg caggaccgca ttccaaactga agatcatccc ttatttgatc ccaacaaacg 180
gtgttgcatg gattcggaat gcggctatcc atgctggcct tgcgtgtatg gataagcttt 240
gttatcgagg cctcatccag tgtcaacgaa taagtaaac gattgcagt 289

<210> 330
<211> 70
<212> PRT
<213> Conus ammiralis

<400> 330
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30
Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
35 40 45
Asp Pro Asn Lys Arg Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys
50 55 60
Trp Pro Cys Cys Tyr Gly
65 70

<210> 331
<211> 16
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i
s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
ue 9 and 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
o-Tyr or O-phospho-Ty

<400> 331
Cys Cys Asp Asp Ser Xaa Cys Gly Xaa Ser Cys Xaa Xaa Cys Cys Xaa
1 5 10 15

<210> 332
<211> 272
<212> DNA
<213> Conus spurius

<400> 332
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccattctgtct 60

gcttctgttt ccaagtactt ctcttccgct ggatggagat caacctgcag tccgatctgc 120
 aaagcgtatg cattcatcta tacagcgtcg tttctttgat cccgtcaaac ggtgttgccc 180
 tagatgcagc gagtgcgaacc cttgttgttg atgaccagct ttgtcatcgc ggcctcatta 240
 agtgtctaata gaataagtaa aatgattgca gt 272

<210> 333
 <211> 63
 <212> PRT
 <213> Conus spurius

<400> 333
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Arg Thr Ser Leu Pro Leu Asp Gly Asp Gln Pro Ala Val Arg Ser
 20 25 30

Ala Lys Arg Met His Ser Ser Ile Gln Arg Arg Phe Phe Asp Pro Val
 35 40 45

Lys Arg Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys Gly
 50 55 60

<210> 334
 <211> 12
 <212> PRT
 <213> Conus spurius

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 3 and 10 is Pro or Hy

<400> 334
 Cys Cys Xaa Arg Cys Ser Xaa Cys Asn Xaa Cys Cys
 1 5 10

<210> 335
 <211> 293
 <212> DNA
 <213> Conus omaria

<400> 335
 caagagggat cगतatgcagt tcatgatgtc taaactggga gtctcgttga ccatctgtct 60
 acttctatatt tcccttaactg ctgttccgct tgatggagat caacatgcag accaactctg 120
 agagcgtctg caggcgacata ttttatctga aaagcatccc ttatttaac cgcgtcaaacg 180
 gtgttgcatg gaggaagaat gcagcagtgat atgctggcct tgtgtgttggg ggtgatcagc 240
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaatgattgc agt 293

<210> 336
 <211> 70
 <212> PRT
 <213> Conus omaria

<400> 336
 Met Met Ser Lys Leu Gly Val Ser Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Cys Thr Pro Cys Asp Cys
65 70

<210> 340
 <211> 17
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue is 14 Pro or Hyp; Xaa at residue 6 is Trp or bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 340
 Cys Cys Lys Xaa Gly Xaa Thr Cys Leu Leu Gly Cys Thr Xaa Cys Asp
 1 5 10 15

Cys

<210> 341
 <211> 290
 <212> DNA
 <213> Conus omaria

<400> 341
 caagagggat cgaatagcagt tcatgatgtc tatactggga gtcttgttga tcatctgtct 60
 acttctgtgt ccccttaactg ctgtttctgga ggatggagat caacctgcag accgacctgc 120
 agagcgtatg caggacggca ttcatctga acatcatccc tttttggatc ccgtcaaacg 180
 gtgttgccat ctattggcat gccgctttgg atgctcgccct tgttgttgtt gaccagcttt 240
 gttatcgcgg cctcatcaag tgtctaatag ataagtaaaa cgattgcagt 290

<210> 342
 <211> 69
 <212> PRT
 <213> Conus omaria

<400> 342
 Met Met Ser Ile Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys
 1 5 10 15
 Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Leu
 35 40 45

Asp Pro Val Lys Arg Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys
 50 55 60

Ser Pro Cys Cys Trp
 65

<210> 343
 <211> 16
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or bromo-Tr

<400> 343
 Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys Xaa
 1 5 10 15

<210> 344
 <211> 293
 <212> DNA
 <213> Conus omaria

<400> 344
 caagaaggat cgaatagcagt tcatgatgtc taaactggga gtcttggtga tcatctgtct 60
 actcttttgt ccccttactg ctgttccgca ggatggagat caacctgcag accgacctgc 120
 agagcgtatg cagggcgcca ttcatctga acatcatccc tttttgac cpgtcaaacg 180
 gtgttgagg tacgggtgga catgctggct aggatgcact ccctgtggtt gttgaccagc 240
 ttgttatcg cgccctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 345
 <211> 70
 <212> PRT
 <213> Conus omaria

<400> 345
 Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys
 1 5 10 15

Pro Leu Thr Ala Val Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Gly Gly Ile Ser Ser Glu His His Pro Phe Phe
 35 40 45

Asp Pro Val Lys Arg Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly
 50 55 60

Cys Thr Pro Cys Gly Cys
 65 70

<210> 346
 <211> 17
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 6 and 9 is Trp or
 bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 346
 Cys Cys Arg Xaa Gly Xaa Thr Cys Xaa Leu Gly Cys Thr Xaa Cys Gly
 1 5 10 15

Cys

<210> 347
 <211> 293
 <212> DNA
 <213> Conus episcopatus

<400> 347
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60
 acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg caggcgacaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg 180
 gtgttgcgat gaggacgaat gcaacagttc atgctggcct tgttgttggg ggtgatcagc 240
 ttgtttatcg cggcctcagc aagtgtataa tgaataagta aaacgattgc agt 293

<210> 348
 <211> 70
 <212> PRT
 <213> Conus episcopatus

<400> 348
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45

Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys
 50 55 60

Trp Pro Cys Cys Trp Gly
 65 70

<210> 349
 <211> 16
 <212> PRT
 <213> Conus episcopatus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residu
 e 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 349
 Cys Cys Asp Xaa Asp Xaa Cys Asn Ser Ser Cys Xaa Xaa Cys Cys Xaa
 1 5 10 15

<210> 350
 <211> 293
 <212> DNA
 <213> Conus episcopatus

<400> 350
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60
 acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg caggcgacaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg 180
 gtgttgcgat gaggacgaat gcacagttc atgctggcct tgttgttggg gatgagcagc 240
 ttgtttatcg cggcctcagc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 351
 <211> 70

<212> PRT
 <213> Conus episcopatus

<400> 351
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45
 Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys
 50 55 60
 Trp Pro Cys Cys Trp Gly
 65 70

<210> 352
 <211> 16
 <212> PRT
 <213> Conus episcopatus
 <220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue4 and 6 is Glu or gamma-carboxy Glu; Xaa at residu
 e 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 352
 Cys Cys Asp Xaa Asp Xaa Cys Ser Ser Ser Cys Xaa Xaa Cys Cys Xaa
 1 5 10 15

<210> 353
 <211> 290
 <212> DNA
 <213> Conus episcopatus

<400> 353
 caagaggggat cgaatgcagt tcaatgatgtc taaactggga gtcttggtga ccatctgtct 60
 acttctgttt tccottactg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg caggcgaca ttttatctga aaagcatccc ttatttaaat ccgtcaaacg 180
 gtgttgcccg gcggggcat gtgccatggg atgcaagcct tgttggtgat gaggcgttt 240
 gttatcgtgg cctcatcaag tgtctaatga ataagtaaaa cgattgcagt 290

<210> 354
 <211> 69
 <212> PRT
 <213> Conus episcopatus

<400> 354
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45

Asn Pro Val Lys Arg Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys
 50 55 60

Lys Pro Cys Cys Gly
 65

<210> 355
 <211> 15
 <212> PRT
 <213> *Conus episcopat*

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 3 and 13 is Pro or Hyp

<400> 355
 Cys Cys Xaa Ala Ala Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys
 1 5 10 15

<210> 356
 <211> 295
 <212> DNA
 <213> *Conus aulicus*

<400> 356
 caagagggat cgatagcagt tcatgatgtc taaactggga gtctgtgtga ccatctgtct 60
 gcttctgttt tccgttactg ctcttccgcc ggaatggagat caacctgcag accgagctgc 120
 agagcgttagg caggtcgagc agcatcccggt gtttgatcat gaaagagggt gttgctcgcc 180
 accatgccac agtatttgcg ctgctttctg ttgcgggtga tgataacgtg ttgatgaccc 240
 accttgatcat cacggctgcg tcaagtgtct aatgaataag taaatgatt gcagt 295

<210> 357
 <211> 65
 <212> PRT
 <213> *Conus aulicus*

<400> 357
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Val Thr Ala Leu Pro Pro Asp Gly Asp Gln Pro Ala Asp Arg Ala
 20 25 30

Ala Glu Arg Arg Gln Val Glu Gln His Pro Val Phe Asp His Glu Arg
 35 40 45

Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys
 50 55 60

Gly
 65

<210> 358
 <211> 16
 <212> PRT
 <213> *Conus aulicus*

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 5 and 6 is Pro or Hyp

<400> 358

Gly Cys Cys Ser Xaa Xaa Cys His Ser Ile Cys Ala Ala Phe Cys Cys
 1 5 10 15

<210> 359

<211> 290

<212> DNA

<213> Conus aulicus

<400> 359

caagagggat cgaatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

acttctgttt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120

agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaagc 180

gtgttgccga ccgtgggcat gtgccatggg atgcaagcct tgttgtggat gacgagcttt 240

gttatcgtgg cctcatcaag tgtctaataa ataagtaaaa tgattgcagt 290

<210> 360

<211> 69

<212> PRT

<213> Conus aulicus

<400> 360

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45

Asn Pro Val Lys Arg Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys
 50 55 60

Lys Pro Cys Cys Gly
 65

<210> 361

<211> 15

<212> PRT

<213> Conus aulicus

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 361

Cys Cys Arg Xaa Val Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys
 1 5 10 15

<210> 362

<211> 290

<212> DNA

<213> Conus aulicus

<400> 362

caagagggat cgaatagcagt tcatgatgtc taaactggga gtcttgttga tcatctgtct 60

acttctgtct ccccttactg ctgttccgct ggaaggagat caacctgcag accgaacctgc 120

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agagcgtatg caggacgaca ttctatctga acatcaaccc atgtttgatg ccacagaca      180
gtgttgcccg gcggtggcat gcgccatggg atgcgagcct tgttgtggat gaccagcttt      240
gttatcgcg cctcatcaag tgtctaataa ataagtaaa tgattgcagt      290

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<210> 363
<211> 69
<212> PRT
<213> Conus aulicus

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<400> 363
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Ser
1          5          10          15

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Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20          25          30

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Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His Gln Pro Met Phe
35          40          45

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Asp Ala Ile Arg Gln Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys
50          55          60

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Glu Pro Cys Cys Gly
65

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<210> 364
<211> 16
<212> PRT
<213> Conus aulicus

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<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 13 is Glu or
gamma-carboxy Glu; Xaa at residue 4 and 14 is Pro or Hy

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<400> 364
Xaa Cys Cys Xaa Ala Val Ala Cys Ala Met Gly Cys Xaa Xaa Cys Cys
1          5          10          15

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<210> 365
<211> 293
<212> DNA
<213> Conus aureus

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<400> 365
caagaaggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccactctgtct      60
acttctgttt tcccttactg ctgttcgctg ggtatgggat caacatgcag accaacatgc      120
agagcgtctg catgaccgcc ttccaactga aaatcatccc ttatatgac cgtcaaaacg      180
gtgttgcgat gattcggaat gcgactatcc ttgtcggcct tgctgtattt ttggataacc      240
tttgttatcg cggcctcatc aagtgtcaaa tgaataagta aaacgattgc agt      293

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<210> 366
<211> 71
<212> PRT
<213> Conus aureus

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<400> 366

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Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln His
20 25 30

Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50 55 60

Trp Pro Cys Cys Ile Phe Gly
65 70

<210> 367

<211> 17

<212> PRT

<213> Conus aureus

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 367

Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
1 5 10 15

Phe

<210> 368

<211> 290

<212> DNA

<213> Conus aureus

<400> 368 caagagggat ccatgacagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60

acttctgttt tccctaaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120

agagcgtctg caggaccgca ttccaactga aaatcatccc ttatttgatc cgaacaaaag 180

gtgttgcaat gattgggaat gcgacgattc atgctggcct tgctgttatg gataaccttt 240

gttatcgcg gctcatcaag tgtcaaatga ataagtaaaa cgattgcagt 290

<210> 369

<211> 70

<212> PRT

<213> Conus aureus

<400> 369

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asn His Pro Leu Phe
35 40 45

Asp Pro Asn Lys Arg Cys Cys Asn Asp Trp Glu Cys Asp Asp Ser Cys
50 55 60

Trp Pro Cys Cys Tyr Gly
65 70

<210> 370
<211> 16
<212> PRT
<213> Conus aureus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 5 and 12 is Trp or bromo-Trp; Xaa at residue 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 370
Cys Cys Asn Asp Xaa Xaa Cys Asp Asp Ser Cys Xaa Xaa Cys Cys Xaa
1 5 10 15

<210> 371
<211> 310
<212> DNA
<213> Conus consors

<400> 371
caagagggat cgaatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgttt 60
gtctctgttt ccccttactg ctcttccaat ggatggagat caatctgtag accgacctgc 120
agagcgtatg caggacgaca ttcatctga gctgcatccc ttgttcaatc agaaaaaagt 180
gtgttgccgc gaaggtgcgc catgccccag ctatttcaga aacagtcaga ttgttcattg 240
ttgttaaagt acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa 300
tgattgcagt 310

<210> 372
<211> 74
<212> PRT
<213> Conus consors

<400> 372
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Phe
35 40 45

Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr
50 55 60

Phe Arg Asn Ser Gln Ile Cys His Cys Cys
65 70

<210> 373
<211> 22
<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 373

Met Cys Cys Gly Xaa Gly Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
1 5 10 15

Gln Ile Cys His Cys Cys
20

<210> 374

<211> 315

<212> DNA

<213> Conus consors

<400> 374

taagagggat cgatagcagt tcgatgtgc taaactggga gtcttgttga ccattctgtct 60
gtctctgttt ccccttattg ctcttccaat ggatggagat caacctgcag accgacctgc 120
agagcgtatg caggacgaca ttctcatctca gcagcatccc ttgtttgata agagaggcgg 180
ctgttgcgat gtgccgaacg catgctccgg cagatgggtgc agagatcacg cacaatgttg 240
cggatgacga taactgtgtg atgaccaact ttgtgatcac ggctacatca agtgaataag 300
taaaacgatt gcagt 315

<210> 375

<211> 74

<212> PRT

<213> Conus consors

<400> 375

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
1 5 10 15

Pro Leu Ile Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Gln Gln His Pro Leu Phe
35 40 45

Asp Lys Arg Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg
50 55 60

Trp Cys Arg Asp His Ala Gln Cys Cys Gly
65 70

<210> 376

<211> 22

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Tr

<400> 376
 Gly Arg Cys Cys Asp Val Xaa Asn Ala Cys Ser Gly Arg Xaa Cys Arg
 1 5 10 15
 Asp His Ala Gln Cys Cys
 20
 <210> 377
 <211> 322
 <212> DNA
 <213> Conus consors
 <400> 377
 caagagggat c gatagcagt tcatgatgtc taaactggga gtcttgttga ctgtctgttt 60
 gcttctgttt ccccttactg ctcttccgat ggatggagat caacctgcag accaacctgc 120
 agagcgtatg caggacgaca ttctatctga gcagcatccc ttgtttgata agagacaaaag 180
 gtgttgcaact gggaagaagg ggtcatgctc cggtaaagca tgcaaaagtc tcaaatgttg 240
 ctctggacga taacgtgttg atgaccaact ttgttatcac ggctacgtca agtgtctagt 300
 gaataagtaa aacgattgca gt 322
 <210> 378
 <211> 76
 <212> PRT
 <213> Conus consors
 <400> 378
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe
 35 40 45
 Asp Lys Arg Gln Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly
 50 55 60
 Lys Ala Cys Lys Ser Leu Lys Cys Cys Ser Gly Arg
 65 70 75
 <210> 379
 <211> 23
 <212> PRT
 <213> Conus consors
 <220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu
 <400> 379
 Xaa Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15
 Lys Ser Leu Lys Cys Cys Ser
 20
 <210> 380

<211> 284
 <212> DNA
 <213> Conus emaciatus

<400> 380
 caagagggat cgaatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct 60
 gcttctgttt ccccttactg ttcttcggat ggatggagat caacctgcag acctactgc 120
 attgcgtgcg cagttctttg cacctgaaca tagtccccgg ttgaccccg tcaaacggtg 180
 ctgctcgcgg gattgcagtg ttgcatccc ttgttgcccg tatggatcac cttgattatt .240
 ggggccagct caagtgtcta atgaataagt aaaatgattg cagt 284

<210> 381
 <211> 70
 <212> PRT
 <213> Conus emaciatus

<400> 381
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Val Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Leu Pro
 20 25 30
 Ala Leu Arg Ala Gln Phe Phe Ala Pro Glu His Ser Pro Arg Phe Asp
 35 40 45
 Pro Val Lys Arg Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys
 50 55 60
 Cys Pro Tyr Gly Ser Pro
 65 70

<210> 382
 <211> 18
 <212> PRT
 <213> Conus emaciatus

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 11, 14 and 18 is Pro or Hyp; Xaa at residue 15 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
 pho-Ty

<400> 382
 Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Xaa Cys Cys Xaa Xaa Gly
 1 5 10 15

Ser Xaa

<210> 383
 <211> 13
 <212> PRT
 <213> Conus aurisiacus

<400> 383
 Cys Cys Lys Val Gln Cys Glu Ser Cys Thr Pro Cys Cys
 1 5 10

<210> 384
 <211> 15

<212> PRT
 <213> Conus atlanticus

<400> 384
 Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe Cys Val Pro Cys Cys
 1 5 10 15

<210> 385
 <211> 14
 <212> PRT
 <213> Conus arentus

<400> 385
 Cys Cys Glu Arg Pro Cys Asn Ile Gly Cys Val Pro Cys Cys
 1 5 10

<210> 386
 <211> 16
 <212> PRT
 <213> Conus bandus

<400> 386
 Cys Cys Asn Trp Pro Cys Ser Met Gly Cys Ile Pro Cys Cys Tyr Tyr
 1 5 10 15

<210> 387
 <211> 15
 <212> PRT
 <213> Conus betulinus

<400> 387
 Cys Cys Glu Leu Pro Cys His Gly Cys Val Pro Cys Cys Trp Pro
 1 5 10 15

<210> 388
 <211> 16
 <212> PRT
 <213> Conus betulinus

<400> 388
 Cys Cys Gly Leu Pro Cys Asn Gly Cys Val Pro Cys Cys Trp Pro Ser
 1 5 10 15

<210> 389
 <211> 18
 <212> PRT
 <213> Conus betulinus

<400> 389
 Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Pro Cys Cys Pro Asn Trp
 1 5 10 15

Pro Ala

<210> 390
 <211> 14
 <212> PRT
 <213> Conus betulinus

<400> 390
 Cys Cys Lys Gln Ser Cys Thr Thr Cys Met Pro Cys Cys Trp
 1 5 10

<210> 391
 <211> 14

<212> PRT
 <213> Conus betulinus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa is Glu or gamma-carboxy Glu

<400> 391
 Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Pro Cys Cys
 1 5 10

<210> 392
 <211> 14
 <212> PRT
 <213> Conus betulinus

<400> 392
 Cys Cys Glu Gln Ser Cys Thr Thr Cys Met Pro Cys Cys Trp
 1 5 10

<210> 393
 <211> 18
 <212> PRT
 <213> Conus characteristicus

<400> 393
 Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser Cys His Gly Ser Cys Cys
 1 5 10 15

Tyr Lys

<210> 394
 <211> 15
 <212> PRT
 <213> Conus characteristicus

<400> 394
 Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Lys Pro Cys Cys
 1 5 10 15

<210> 395
 <211> 17
 <212> PRT
 <213> Conus characteristicus

<400> 395
 Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Met
 1 5 10 15

Phe

<210> 396
 <211> 14
 <212> PRT
 <213> Conus characteristicus

<400> 396
 Cys Cys Arg Arg Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
 1 5 10

<210> 397
 <211> 16
 <212> PRT
 <213> Conus textile

<400> 397
 Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Lys Pro Cys Cys Gly
 1 5 10 15

<210> 398
 <211> 19
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa is Hyp

<400> 398
 Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa
 1 5 10 15

Cys Cys Asn

<210> 399
 <211> 15
 <212> PRT
 <213> Conus capitaneus

<400> 399
 Ser Cys Cys Arg Asp Cys Gly Glu Asp Cys Val Gly Cys Cys Arg
 1 5 10 15

<210> 400
 <211> 16
 <212> PRT
 <213> Conus coronatus

<400> 400
 Cys Cys Asp Trp Pro Cys Ile Pro Gly Cys Thr Pro Cys Cys Leu Pro
 1 5 10 15

<210> 401
 <211> 18
 <212> PRT
 <213> Conus dalli

<400> 401
 Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile
 1 5 10 15

Leu Ser

<210> 402
 <211> 17
 <212> PRT
 <213> Conus dalli

<400> 402
 Glx Gln Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Glu Pro Cys
 1 5 10 15

Cys

<210> 403
 <211> 16
 <212> PRT
 <213> Conus dalli

<400> 403
 Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Pro Cys Cys Trp
 1 5 10 15

<210> 404
 <211> 14
 <212> PRT
 <213> Conus distans

<400> 404
 Glx Cys Cys Val His Pro Cys Pro Cys Thr Pro Cys Cys Arg
 1 5 10

<210> 405
 <211> 14
 <212> PRT
 <213> Conus figulinus

<400> 405
 Cys Cys Pro Trp Pro Cys Asn Ile Gly Cys Val Pro Cys Cys
 1 5 10

<210> 406
 <211> 14
 <212> PRT
 <213> Conus figulinus

<400> 406
 Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro Cys Cys Pro
 1 5 10

<210> 407
 <211> 15
 <212> PRT
 <213> Conus figulinus

<400> 407
 Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu
 1 5 10 15

<210> 408
 <211> 16
 <212> PRT
 <213> Conus figulinus

<400> 408
 Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro Cys Cys Thr Ser
 1 5 10 15

<210> 409
 <211> 16
 <212> PRT
 <213> Conus figulinus

<400> 409
 Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro Cys Cys Ile Pro
 1 5 10 15

<210> 410
 <211> 16
 <212> PRT
 <213> Conus generalis

<400> 410

Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro
 1 5 10 15

<210> 411
 <211> 16
 <212> PRT
 <213> Conus generalis

<400> 411
 Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Leu Thr
 1 5 10 15

<210> 412
 <211> 16
 <212> PRT
 <213> Conus generalis

<400> 412

Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro
 1 5 10 15

<210> 413
 <211> 17
 <212> PRT
 <213> Conus gloriamaris

<400> 413
 Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Met
 1 5 10 15

Phe

<210> 414
 <211> 17
 <212> PRT
 <213> Conus gloriamaris

<400> 414
 Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys
 1 5 10 15
 Trp

<210> 415
 <211> 16
 <212> PRT
 <213> Conus gloriamaris

<400> 415
 Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys Gly
 1 5 10 15

<210> 416
 <211> 13
 <212> PRT
 <213> Conus laterculatus

<400> 416
 Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys Cys
 1 5 10

<210> 417
 <211> 19
 <212> PRT
 <213> Conus leopardus

<400> 417
 Glx Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr Cys Arg His Gln
 1 5 10 15

Cys Cys His

<210> 418
 <211> 19
 <212> PRT
 <213> Conus lividus

<400> 418
 Glx Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser Cys His Tyr Gln
 1 5 10 15

Cys Cys His

<210> 419
 <211> 14
 <212> PRT
 <213> Conus marmoreus

<400> 419
 Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His Pro Cys Cys
 1 5 10

<210> 420
 <211> 17
 <212> PRT
 <213> Conus marmoreus

<400> 420
 Glu Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Pro Cys Cys
 1 5 10 15

Val

<210> 421
 <211> 19
 <212> PRT
 <213> Conus marmoreus

<400> 421
 Ser Lys Gln Cys Cys His Leu Pro Ala Cys Arg Phe Gly Cys Thr Pro
 1 5 10 15

Cys Cys Trp

<210> 422
 <211> 17
 <212> PRT
 <213> Conus marmoreus

<400> 422
 Met Gly Cys Cys Pro Phe Pro Cys Lys Thr Ser Cys Thr Thr Leu Cys
 1 5 10 15

Cys

<210> 423
 <211> 14
 <212> PRT
 <213> Conus musicus

<400> 423

Ala Cys Cys Glu Gln Ser Cys Thr Thr Cys Phe Pro Cys Cys
1 5 10

<210> 424
<211> 15
<212> PRT
<213> Conus nobilis

<400> 424
Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe Cys Val Pro Cys Cys
1 5 10 15

<210> 425
<211> 14
<212> PRT
<213> Conus pulicarius

<400> 425
Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10

<210> 426
<211> 17
<212> PRT
<213> Conus quercinus

<400> 426
Glx Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg
1 5 10 15

Thr

<210> 427
<211> 18
<212> PRT
<213> Conus quercinus

<400> 427
Glx Arg Cys Cys Arg Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg
1 5 10 15

Tyr Arg

<210> 428
<211> 18
<212> PRT
<213> Conus quercinus

<400> 428
Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser Cys His Gly Ser Cys Cys
1 5 10 15

Tyr Lys

<210> 429
<211> 15
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa is Hyp

<400> 429

Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Pro Asn
1 5 10 15

<210> 430
<211> 15
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa is Hyp

<400> 430
Cys Cys Ser Arg His Cys Trp Val Cys Ile Xaa Cys Cys Pro Asn
1 5 10 15

<210> 431
<211> 16
<212> PRT
<213> Conus rattus

<400> 431
Glx Thr Cys Cys Ser Asn Cys Gly Glu Asp Cys Asp Gly Cys Cys Gln
1 5 10 15

<210> 432
<211> 20
<212> PRT
<213> Conus striatus

<400> 432
Glx Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Trp Cys Arg Asp His
1 5 10 15

Ala Arg Cys Cys
20

<210> 433
<211> 12
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(12)
<223> Xaa is Hyp

<400> 433
Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys
1 5 10

<210> 434
<211> 14
<212> PRT
<213> Conus tessulatus

<400> 434
Cys Cys His Lys Cys Tyr Met Gly Cys Ile Pro Cys Cys Ile
1 5 10

<210> 435
<211> 18
<212> PRT
<213> Conus tessulatus

<400> 435
 Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Tyr

<210> 436
 <211> 23
 <212> PRT
 <213> Conus betulinus

<400> 436
 Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Phe Val Met Ile Thr Cys
 20

<210> 437
 <211> 23
 <212> PRT
 <213> Conus betulinus

<400> 437
 Arg Cys Cys Arg Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Phe Val Met Ile Thr Cys
 20

<210> 438
 <211> 15
 <212> PRT
 <213> Conus textile

<400> 438
 Phe Cys Cys Asp Ser Asn Trp Cys His Asp Cys Glu Cys Cys Tyr
 1 5 10 15

<210> 439
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<400> 439
 Cys Cys His Trp Asn Trp Cys Asp His Leu Cys Ser Cys Cys Gly Ser
 1 5 10 15

<210> 440
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa is Hyp

<400> 440
 Asp Cys Cys Xaa Leu Pro Ala Cys Pro Phe Gly Cys Asn Xaa Cys Cys
 1 5 10 15

<210> 441
 <211> 16

<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa is Hyp

<400> 441
Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
1 5 10 15

<210> 442
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa is Hyp

<400> 442
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
1 5 10 15

<210> 443
<211> 16
<212> PRT
<213> Conus marmoreus

<400> 443
Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Pro Cys Cys Arg
1 5 10 15

<210> 444
<211> 17
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa is Hyp

<400> 444
Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
1 5 10 15

Val

<210> 445
<211> 15
<212> PRT
<213> Conus textile

<400> 445
Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys
1 5 10 15

<210> 446
<211> 16
<212> PRT
<213> Conus textile

<400> 446
Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu Cys Cys
1 5 10 15

<210> 447
<211> 17
<212> PRT
<213> Conus aureus

<400> 447
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile
1 5 10 15

Phe

<210> 448
<211> 16
<212> PRT
<213> Conus aureus

<400> 448
Cys Cys Asn Asp Trp Glu Cys Asp Asp Ser Cys Trp Pro Cys Cys Tyr
1 5 10 15

<210> 449
<211> 16
<212> PRT
<213> Conus ammiralis

<400> 449
Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys
1 5 10 15

<210> 450
<211> 12
<212> PRT
<213> Conus ammiralis

<400> 450
Cys Cys Met Thr Cys Phe Gly Cys Thr Pro Cys Cys
1 5 10

<210> 451
<211> 18
<212> PRT
<213> Conus ammiralis

<400> 451
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile
1 5 10 15

Phe Ser

<210> 452
<211> 13
<212> PRT
<213> Conus ammiralis

<400> 452
Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Pro Cys Cys
1 5 10

<210> 453
<211> 16
<212> PRT

<213> Conus ammiralis

<400> 453

Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys Trp Pro Cys Cys Tyr
1 5 10 15

<210> 454

<211> 16

<212> PRT

<213> Conus aulicus

<400> 454

Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys
1 5 10 15

<210> 455

<211> 15

<212> PRT

<213> Conus aulicus

<400> 455

Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys Lys Pro Cys Cys
1 5 10 15

<210> 456

<211> 16

<212> PRT

<213> Conus aulicus

<400> 456

Glx Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys Glu Pro Cys Cys
1 5 10 15

<210> 457

<211> 18

<212> PRT

<213> Conus emaciatatus

<400> 457

Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys Cys Pro Tyr Gly
1 5 10 15

Ser Pro

<210> 458

<211> 16

<212> PRT

<213> Conus episcopatus

<400> 458

Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys Trp Pro Cys Cys Trp
1 5 10 15

<210> 459

<211> 16

<212> PRT

<213> Conus episcopatus

<400> 459

Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys Trp Pro Cys Cys Trp
1 5 10 15

<210> 460

<211> 15

<212> PRT

<213> Conus episcopatus

<400> 460

Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys Lys Pro Cys Cys
1 5 10 15

<210> 461

<211> 16

<212> PRT

<213> Conus omaria

<400> 461

Cys Cys Asp Glu Glu Glu Cys Ser Ser Ala Cys Trp Pro Cys Cys Trp
1 5 10 15

<210> 462

<211> 16

<212> PRT

<213> Conus omaria

<400> 462

Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys Trp
1 5 10 15

<210> 463

<211> 12

<212> PRT

<213> Conus spurius

<400> 463

Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys
1 5 10

<210> 464

<211> 16

<212> PRT

<213> Conus pennaceus

<400> 464

Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys
1 5 10 15

<210> 465

<211> 19

<212> PRT

<213> Conus flavidus

<400> 465

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Ser Ser

<210> 466

<211> 14

<212> PRT

<213> Conus pulicarius

<400> 466

Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys Cys His Ile
1 5 10

<210> 467

<211> 15

<212> PRT

<213> Conus ebraceus

<400> 467
Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10 15

<210> 468
<211> 15
<212> PRT
<213> Conus ebraceus

<400> 468
Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10 15

<210> 469
<211> 14
<212> PRT
<213> Conus pulicarius

<400> 469
Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10

<210> 470
<211> 16
<212> PRT
<213> Conus miliaris

<400> 470
Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro Cys Cys Phe Pro
1 5 10 15

<210> 471
<211> 16
<212> PRT
<213> Conus miliaris

<400> 471
Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys Phe Arg
1 5 10 15

<210> 472
<211> 23
<212> PRT
<213> Conus rattus

<400> 472
Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys Lys
1 5 10 15

Pro Ala Arg Cys Cys Gly Pro
20

<210> 473
<211> 22
<212> PRT
<213> Conus stercusmuscarum

<400> 473
Glx Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Trp Cys Arg
1 5 10 15

Asp His Ser Arg Cys Cys
20

<210> 474
 <211> 22
 <212> PRT
 <213> Conus consors

<400> 474
 Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg Trp Cys Arg
 1 5 10 15
 Asp His Ala Gln Cys Cys
 20

<210> 475
 <211> 23
 <212> PRT
 <213> Conus consors

<400> 475
 Glx Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15
 Lys Ser Leu Lys Cys Cys Ser
 20

<210> 476
 <211> 22
 <212> PRT
 <213> Conus aurisiacus

<400> 476
 Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr Phe Arg Asn Ser
 1 5 10 15
 Gln Ile Cys His Cys Cys
 20

<210> 477
 <211> 19
 <212> PRT
 <213> Conus aurisiacus

<400> 477
 Cys Cys Arg Trp Pro Cys Pro Arg Gln Ile Asp Gly Glu Tyr Cys Gly
 1 5 10 15
 Cys Cys Leu

<210> 478
 <211> 22
 <212> PRT
 <213> Conus bullatus

<400> 478
 Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr Trp Lys Asn Ser
 1 5 10 15
 Gln Ile Cys Ala Cys Cys
 20

<210> 479
 <211> 21
 <212> PRT
 <213> Conus characteristicus

<400> 479

Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp Asn Phe
 1 5 10 15

Ile Cys Gly Cys Cys
 20

<210> 480
 <211> 23
 <212> PRT
 <213> Conus circumciscus

<400> 480
 Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr Phe Lys Asp
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
 20

<210> 481
 <211> 20
 <212> PRT
 <213> Conus ermineus

<400> 481
 Cys Cys Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys
 1 5 10 15

Phe Cys Cys Leu
 20

<210> 482
 <211> 21
 <212> PRT
 <213> Conus magus

<400> 482
 Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp Asn Phe
 1 5 10 15

Ile Cys Gly Cys Cys
 20

<210> 483
 <211> 22
 <212> PRT
 <213> Conus magus

<400> 483
 Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser
 1 5 10 15

Gln Ile Cys His Cys Cys
 20

<210> 484
 <211> 22
 <212> PRT
 <213> Conus magus

<400> 484
 Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Thr Asp
 1 5 10 15

Asn Phe Ile Cys Gly Cys
 20

<210> 485
 <211> 23
 <212> PRT
 <213> Conus magus

<400> 485
 Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
 20

<210> 486
 <211> 23
 <212> PRT
 <213> Conus striatus

<400> 486
 Glx Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe Lys Asn
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
 20

<210> 487
 <211> 22
 <212> PRT
 <213> Conus magus

<400> 487
 Glx Lys Cys Cys Ser Gly Gly Ser Cys Pro Leu Tyr Phe Arg Asp Arg
 1 5 10 15

Leu Ile Cys Pro Cys Cys
 20

<210> 488
 <211> 23
 <212> PRT
 <213> Conus stercusmuscarum

<400> 488
 Glx Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe Lys Asp
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
 20

<210> 489
 <211> 22
 <212> PRT
 <213> Conus consors
 <400> 489

Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser
 1 5 10 15

Gln Ile Cys His Cys Cys
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<210> 490
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